

GenCore version 4.5  
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## OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 15:10:37 : Search time 5976.93 Seconds  
(Without alignments)  
5756.003 Million cell updates/sec

Title: US-09-581-241-3  
Perfect score: 1644  
Sequence: 1 atggaataacatgagagaacga.....agaacacgttgctaagatg 1644

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

GenBank: \*  
1: gb\_ba: \*  
2: gb\_bg: \*  
3: gb\_in: \*  
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6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
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27: em\_sts: \*  
28: em\_un: \*  
29: em\_vl: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htg\_inv: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	1644	100.0	1644	6	E36479	E36479 Luciferase
2	1640.8	99.8	1644	6	E36480	E36480 Luciferase
3	1639.2	99.7	1644	6	AR098258	AR098258 Sequence
4	1636	99.5	1644	6	E02495	E02495 cDNA encodi
5	1636	99.5	1644	6	E05448	E05448 cDNA sequen
6	1636	99.5	1781	6	LLUC1	X66919 L. lateralis
7	1631.4	99.2	1908	6	AR043317	AR043317 Sequence
8	1631.4	99.2	1908	6	AR062709	AR062709 Sequence
9	1631.4	99.2	1908	6	E12279	E12279 cDNA encodi
10	1631.4	99.2	1920	6	E16288	E16288 DNA encodin
11	1623.2	98.7	2019	23	E10169	E10169 DNA encodin
12	1623.2	98.7	2055	23	E10170	E10170 DNA encodin
13	1622.8	98.7	1704	6	AR043316	AR043316 Sequence
14	1622.8	98.7	1704	6	AR062708	AR062708 Sequence
15	1622.8	98.7	1704	6	E12278	E12278 cDNA encodi
16	1622.8	98.7	1704	6	E13411	E13411 cDNA encodi
17	1621.6	98.6	2364	6	E13412	E13412 cDNA encodi
18	1356	82.5	1644	6	AR108849	AR108849 Sequence
19	1356	82.5	1644	6	AR119318	AR119318 Sequence
20	1356	82.5	1644	6	AR151719	AR151719 Sequence
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22	1356	82.5	1644	6	E01857	E01857 DNA encodin
23	1356	82.5	1644	6	E02267	E02267 cDNA encodi
24	1356	82.5	1644	6	E03259	E03259 cDNA encodi
25	1356	82.5	1644	6	E05447	E05447 cDNA sequen
26	1356	82.5	1985	3	FELUJC	M26194 Luciola cru
27	1263.2	76.8	1566	6	AR098254	AR098254 Sequence
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29	1188.2	72.3	2850	3	LLUCIFPMJ	Z49891 L.lateralis
30	1187.8	72.3	4233	3	LLUCIFS	Z69619 L.lateralis
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34	1040.8	63.3	1656	6	AR098255	AR098255 Sequence
35	1016	61.8	1958	3	HOTLUCT	L39929 Hotaria par
36	1016	61.8	1970	23	E10030	E10030 cDNA coding
37	1014.4	61.7	2009	3	S61961	S61961 Luciferase
38	818.8	49.8	1725	3	LNLUCCPROT	X89479 L.noctiluca
39	789.4	48.0	1647	3	AF328553	AF328553 Pyrococell
40	781.4	47.5	1922	3	PBLUCIF	L39928 Pyrococella
41	745.2	45.3	1773	3	PP911ACNP	X84848 P.pyralis 1
42	745.2	45.3	1811	6	A37556	A37556 Sequence 22
43	745.2	45.3	4672	12	CVE277960	AJ277960 Cloning v
44	745.2	45.3	4674	12	XX002437	U02437 Cloning vec
45	745.2	45.3	5067	12	AF093685	AF093685 Luciferas

## ALIGNMENTS

RESULT 1  
LOCUS E36479  
DEFINITION Luciferase and method for assaying intracellular ATP by using the same.  
ACCESSION E36479  
VERSION E36479.1 GI:13022686  
KEYWORDS JP 1999239493-A/3.  
SOURCE JP 1999239493-A/3.  
ORGANISM Luciola lateralis.  
Luciola lateralis.  
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Coleoptera: Polyphaga: Elateriformia: Cantharoidae: Lampyridae: Luciola.

REFERENCE 1 (bases 1 to 1644)  
Noriaki,H.S.M.M.

AUTHORS Luciferase and method for assaying intracellular ATP by using the  
TITLE Patent: JP 1999239493-A 3 07-SEP-1999;  
JOURNAL KIRKMAN CORP

COMMENT OS Luciola lateralis  
PN JP 1999239493-A/3  
PD 07-SEP-1999  
PF 21-DEC-1998 JP 1998363108  
PR

PC	NORIaki HATTORI, SELJI MURAKAMI
PI	C12N15/09,C12N9/02,C12Q1/66//C12N9/02,C12R1/19,C12N15/00 CC
PH	
FT	
FEATURES	
source	Location/Qualifiers (1):(1644). 1.:1644 /organism="Luciola lateralis" /db_xref="taxon:7052"
BASE COUNT	528 a 261 c 349 g 506 t
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QY	721	acgtgtagtaccattccataatggttttggtatgatttaacttaactttaggtctataactg	780
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QY	781	ggttttcgtatgtcatgatttaacgaatttgacgaagagacgtttttttaaanaacatgcgaa	840
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Db	1621	CTGAAGAAACCAAGTGTCTAAGATG 1644	

RESULT	2
LOCUS	E36480 1644 bp DNA linear PAT 07-FEB-2001
DEFINITION	Luciferase and method for assaying intracellular ATP by using the same.
ACCESSION	E36480
VERSION	E36480.1 GI:13022687
KEYWORDS	JP 1999239493-A/4.
SOURCE	Luciola lateralis.
ORGANISM	Luciola lateralis
REFERENCE	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidea; Lampyridae; Luciola.
AUTHORS	1 (bases 1 to 1644)
TITLE	Noriaki,H.S.M.M.
	Luciferase and method for assaying intracellular ATP by using the

JOURNAL Patent: JP 1999239493-A 4 07-SEP-1999;  
KIKKOMAN CORP  
COMMENT OS Luciola lateralis  
PN JP 1999239493-A/4  
PD 07-SEP-1999  
PE 21-DEC-1998 JP 1998363108  
PR  
PI NORIKI HATTORI, SEIJI MURAKAMI  
PC C12N15/09, C12N9/02, C1201/66, C12N9/02, C12R1:19, C12N15/00 CC

FEATURES FH Key Location/Qualifiers  
FT CDS (1) (1644)  
1.1644  
/organism="Luciola lateralis"  
/db\_xref="taxon:7052"

BASE COUNT 529 a 262 c 348 g 505 t  
ORIGIN

Query Match 99.88; Score 1640.8; DB 6; Length 1644;  
Best Local Similarity 99.98; Pred. No. 0;  
Matches 1642; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1621 ctgaagaacacagttgctaaagt 1644  
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RESULT 3  
AR098258 1644 bp DNA linear PAT 14-FEB-2001  
LOCUS AR098258 Sequence 13 from patent US 6074859.  
DEFINITION AR098258  
ACCESSION AR098258.1 GI:12807515  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
1 (bases 1 to 1644)  
Hirokawa, K., Kajiyama, N. and Murakami, S.  
TITLE  
Mutant-type bioluminescent protein and process for producing the  
JOURNAL  
Patent: US 6074859-A 13 13-JUN-2000;  
FEATURES  
Location/Qualifiers  
1..1644  
BASE COUNT 528 a 260 c 350 g 506 t  
ORIGIN

Query Match 99.7%; Score 1639.2; DB 6; Length 1644;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1641; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 961 ttatctaaagaanaatttggtagagctgttgcacagcgttttaattaccgggtgttcgtca 1020  
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DEFINITION CDNA encoding luciferase.  
ACCESSION E02495  
VERSION E02495.1 GI:2170725  
KEYWORDS JP 1990171189-A/1.  
SOURCE  
ORGANISM  
Luciola lateralis.  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
Elateriformia; Cantharoidae; Lampyridae; Luciola.  
REFERENCE  
1 (bases 1 to 1644)  
AUTHORS  
Kajiyama, N., Tatsumi, H. and Nakano, E.  
TITLE  
LUCIFERASE GENE  
JOURNAL  
Patent: JP 1990171189-A 1 02-JUL-1990;



COMMENT KIKKOMAN CORP  
OS Luciola lateralis  
PN JP 1990171189-A/1  
PD 02-JUL-1990  
PF 22-DEC-1988 JP 1988322029  
PI KAIJIYAMA NAOKI, TATSUMI HIROKI, NAKANO EIICHI PC  
C12N15/53//C12N9/02:  
CC strandedness: Single:  
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FEATURES  
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BASE COUNT 529 a 262 c 349 g 504 t  
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Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 121 gcaattgcttactaagcaactaccggtgctgactaiaagtaacgtaacccgaactaaga 180  
DB 121 GCAATTGCTTACTAAGCAACTACCGGTGCCTGACTAIAAGTAACGTAACCCGAACCTAAGA 180  
QY 181 aaatcagctgtctagagagagcttaagaataatggttgggtgtgtatgaggaagatt 240  
DB 181 AAATCAGCTGTCTAGAGAGAGCTTTAAGAATAATGGTGGTGTGTGATGAGGAAGATT 240  
QY 241 ggcattcagtgaaactgtgaagaattcttattctcctgataagccggttattata 300  
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QY 301 ggtgcgtgtgtgctccaactaagatlttaactctactcgttgaattggttcaagttta 360  
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DB 1141 AAAAAAATCTTGGCCCGGACAGACGCGTGAAGATTGTGTAAGGCTCTTATGCTTATG 1200  
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DB 1621 CTGAAGAACAACGTTGCTAAGATG 1644

RESULT 5  
E05448 E05448 1644 bp RNA linear PAT 29-SEP-1997  
LOCUS DEFINITION CDNA sequence of luciferase.  
ACCESSION E05448  
VERSION E05448.1 GI:2173637

KEYWORDS JP 1993244942-A/2.  
SOURCE Luciola lateralis.  
ORGANISM Luciola lateralis  
REFERENCE Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
AUTHORS pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
TITLE 1 (bases 1 to 1644)  
Kajiyama, N. and Nakano, E.  
HEAT-STABLE FIREFLY LUCIFERASE, HEAT-STABLE FIREFLY LUCIFERASE  
GENE, NEW RECOMBINANT DNA AND PRODUCTION OF HEAT-STABLE FIREFLY  
LUCIFERASE  
JOURNAL Patent: JP 1993244942-A 2 24-SEP-1993;  
COMMENT KIRKOMAN CORP  
OS Luciola lateralis  
PN JP 1993244942-A/2  
PD 24-SEP-1993  
PE 22-MAY-1992 JP 1992131057  
PR 27-JUN-1991 JP 91P 157117, 29-NOV-1991 JP 91P 317064 PI  
PC C12N9/02,C12N15/53/C12N1/21,(C12N9/02,C12N1:19); CC  
Kajiyama NAKOI, NAKANO EICHI  
strandedness: Double;  
CC topology: linear;  
CC hypothetical: No;  
FH anti-sense: No; location/Qualifiers  
FH Key location/Qualifiers  
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source location/Qualifiers  
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BASE COUNT 529 a 262 c 349 g 504 t  
ORIGIN

Query Match 99.5%; Score 1636; DB 6; Length 1644;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 6  
LLOCUS LLOCUC 1781 bp mRNA linear INV 24-NOV-1993  
DEFINITION L. lateralis luciferase mRNA.  
ACCESSION X66919.338389  
VERSION X66919.1 GI:9526  
KEYWORDS luciferase.  
SOURCE Japanese firefly.  
ORGANISM L. lateralis  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
Elateriformia; Cantharoidea; Lampyridae; Luciola.  
1 (bases 1 to 1781)  
REFERENCE 1 Tatsumi, H., Kaijima, N. and Nakano, E.  
TITLE Molecular cloning and expression in Escherichia coli of a CDNA  
JOURNAL clone encoding luciferase of a firefly, Luciola lateralis  
MEDLINE Biochim. Biophys. Acta 1131 (2), 161-165 (1992)  
92305054  
REFERENCE 2 (bases 1 to 1781)  
Tatsumi, H.  
TITLE Direct Submission  
JOURNAL Submitted (21-JUL-1992) H. Tatsumi, Research and Development  
AUTHORS Division, Kikkoman Corporation, 399 Noda, Noda City, Chiba 278,  
JAPAN

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BASE COUNT 579 a 276 c 367 g 559 t  
ORIGIN

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Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY	1441	gaagctccggagagcgtgtttgttacctaaagaagaaatactatgactaaagaaga	1500
Db	1499	GAGCTTCCGGGAGCGCTGTTCTTACTTGAAAAAGGAAATCTATGACTGAAAGAGATTA	1558
QY	1501	atggaattacgttgcgtagtcgaagtttcaaatgcaaaagcttgcgtgtgtgttcgattt	1560
Db	1559	ATGGATTACGTTGCTGATGCAACTTTCAAATGCAAAACGTTTCGAGTGtGTTCGCTTTT	1618
QY	1561	gtggacggaagtacctaagaagttcactcgtgtaaatltgacggtlaaagcaattagagaata	1620
Db	1619	GTGGACGAAGTACCTTAAGGCTCTCACTGGTAAATTTAGACGGTAAGCAATTAGAGAAATA	1678
QY	1621	ctgaagaacaaccagttgctcaagtg	1644
Db	1679	CTGAAGAAACCAAGTGTCTAGATG	1702

RESULT	7
AR043317	
LOCUS	AR043317 1908 bp DNA
DEFINITION	Sequence 8 from patent US 5814465.
ACCESSION	AR043317
VERSION	AR043317.1 GI:5964325
	PAT 29-SEP-1999
	Linear

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
1 (bases 1 to 1908)	Ratsumi, H., Fukuda, S., Kikuchi, M. and Koyama, Y.	Biotinlated firefly luciferase, a gene for biotinlated firefly luciferase, a recombinant DNA, a process for producing biotinlated luciferase, and a bioluminescent analysis method	Patent: US 5814465-A 8 29-SEP-1998;	Location/Qualifiers

BASE COUNT	598 a	329 c	426 g	555 t
ORIGIN	/organism="unknown"			

Query Match	99.2%	Score 1631.4	DB 6	Length 1908
Best Local Similarity	99.68%	Pred. No. 0		
Matches 1635; Conservative	0	Mismatches 6	Indels 0	Gaps 0

OY	1	atggaaacacatgaggaagcaagctgaaataattgtagatggtctcgaacatttaccctatt	60
Db	1	ATGGAANAACATGAGAAACGATGAATAATTTGTGTATGTGCTTCAACCATTTTACCCATT	60
OY	61	gaagaaggatctgcttggagacaacatttgcgcaaglatatagatcgatagatgaaaccttga	120
Db	61	GAAGAAGGATCTGCTTGAGACCAATTGCGCAAGTATATGATGATGATATGCAAAACTTGA	120
OY	121	gcaattccttttctaacgcaattaccggtgtcgattatacgttaagccgaatacttagaa	180
Db	121	GCAATTGCTTTTACTTAACGCACTTACCGGTGTGATTATACGTACGCCGAATCTTAGAA	180
OY	181	aaatcattcgtctccttagagaagagcctttaaagaattatgatttggttttgaatgaagaat	240
Db	181	AAATCATCGTCTAGAGAGAGCGCTTTAAACAATTATGTTGGTTGTTGATGAGAAATT	240
OY	241	gcortatgagagtaaacaattgaagaattccttatctccgtatataacgcggttaattlata	300
Db	241	GCGTTATGCACTGAAACCTGTGAAGACTTTTATTATTCGTATTTACCGGTTATTATTAA	300

QY	301	ggatgcggtgtggtgcgcacacaaatgagatataacacctgaagtgaattggtctcaagttta	360
Db	301	ggatgcggtgtggtgcgcacacaaatgagatataacacctgaagtgaattggtctcaagttta	360
QY	361	ggcactcttaagccacacattgctatctagttcttaaaaaagattaga taaagtctaact	420
Db	361	ggcactcttaagccacacattgctatctagttcttaaaaaagattaga taaagtctaact	420
QY	421	gtacaaaaaacygttaacctgctataaaaccaatgttatcttgagcagcaagtgtatat	480
Db	421	gtacaaaaaacygttaacctgctataaaaccaatgttatcttgagcagcaagtgtatat	480
QY	481	agaagtttcaatccatcagagacacttatataaaaaaacctccacaagtttcaagga	540
Db	481	agaagtttcaatccatcagagacacttatataaaaaaacctccacaagtttcaagga	540
QY	541	tcaagttttaaaactgltagaagttaacccgaagaacaaatgtccttaataatgaactct	600
Db	541	tcaagttttaaaactgltagaagttaacccgaagaacaaatgtccttaataatgaactct	600
QY	601	tccgggttcaaccoggtgttgccaaaagtgtaacacttaactgaanaaattggtctactaga	660
Db	601	tccgggttcaaccoggtgttgccaaaagtgtaacacttaactgaanaaattggtctactaga	660
QY	661	ttttctacgcttagagatcccaattataggaacccaagtttcaccagcagcgctatttta	720
Db	661	ttttctacgcttagagatcccaattataggaacccaagtttcaccagcagcgctatttta	720
QY	721	actgttagtaccatctcatcagtttgcttgatgcttctactcttagctatctaactgtg	780
Db	721	actgttagtaccatctcatcagtttgcttgatgcttctactcttagctatctaactgtg	780
QY	781	ggtttcgattgttcacatgttaacgaanaattgacgaagaagaacttlltaaaaaactgtcaa	840
Db	781	ggtttcgattgttcacatgttaacgaanaattgacgaagaagaacttlltaaaaaactgtcaa	840
QY	841	gattacaaatgttcaaacggttatctctgtgacggaacttftgttcaattctttaagaagt	900
Db	841	gattacaaatgttcaaacggttatctctgtgacggaacttftgttcaattctttaagaagt	900
QY	901	gaatctactcga taaatltatltcaacaattagtttgaanaattgcactgtgcgagacact	960
Db	901	gaatctactcga taaatltatltcaacaattagtttgaanaattgcactgtgcgagacact	960
QY	961	ttatcttaagaagaatttgttgaagctgtgtgtcagaagctlltaattacccgggtgttcgcaa	1020
Db	961	ttatcttaagaagaatttgttgaagctgtgtgtcagaagctlltaattacccgggtgttcgcaa	1020
QY	1021	ggcctatggtttaacagaagaacaactctgtgaattatatacaacccggaagaagatataaa	1080
Db	1021	ggcctatggtttaacagaagaacaactctgtgaattatatacaacccggaagaagatataaa	1080
QY	1081	ccaggtgtcttctgycacaaagttgtgccaattttaaagcaaaagttltcgacttgaact	1140
Db	1081	ccaggtgtcttctgycacaaagttgtgccaattttaaagcaaaagttltcgacttgaact	1140
QY	1141	aaaaaacttgggcccgaacagacgtgtgaagaagttgtgtlaaaggttccctatgtctatg	1200
Db	1141	aaaaaacttgggcccgaacagacgtgtgaagaagttgtgtlaaaggttccctatgtctatg	1200
QY	1201	aaaggttatgtagataatccagaagaacaaagaagaatacatagatgaagaagttgtgtg	1260
Db	1201	aaaggttatgtagataatccagaagaacaaagaagaatacatagatgaagaagttgtgtg	1260
QY	1261	cacacagagatatgttggttatcagcttggaagaaaacatttccctatcgttgatcgtgtg	1320
Db	1261	cacacagagatatgttggttatcagcttggaagaaaacatttccctatcgttgatcgtgtg	1320
QY	1321	aagcttcttaatcaaatcaaaagata tcaagtaaccaccgtcgtcaatagaactctgttct	1380
Db	1321	aagcttcttaatcaaatcaaaagata tcaagtaaccaccgtcgtcgtcaatagaactctgttct	1380
QY	1381	ttgcacacatccaatalatttttgatgccggcgctgtgcgtccacatccctatagctggt	1440

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Db 1441 GAGCTTCGGGAGCTGTGTGTACTTGTCAAAAGGAAATATATGACGTAAGAAAGTA 1500  
Oy 1501 atgattcagctgtgactcaagtttcaaatgcaaaccttgctggtgtgtcgtttt 1560  
Db 1501 ATGATTACGTTGCTAGTCAAGTTTCAATGCCAATTCCTTGCGTGTGTGCTGTTT 1560  
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Db 1561 GTGAGCAGAACTAAAGGCTCCTCACTGTAATGACGTTAAAGCAATTAAGAAATA 1620  
Oy 1621 ctgaagaacacagttgtctaa 1641  
Db 1621 CTGAAGAAACCAAGTTGTAG 1641

RESULT 8  
AR062709  
LOCUS AR062709 1908 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 8 from patent US 5843746.  
ACCESSION AR062709  
VERSION AR062709.1 GI:5990400  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1908)  
AUTHORS Tatsumi, H., Fukuda, S., Kikuchi, M. and Koyama, Y.  
TITLE Biotinlated firefly luciferase, a gene for biotinated firefly luciferase, a recombinant DNA, a process for producing biotinated luciferase and a bioluminescent analysis method  
JOURNAL Patent: US 5843746-A 8 01-DEC-1998;  
FEATURES  
Location/Qualifiers  
source 1..1908  
BASE COUNT 598 a 329 c 426 g 555 t  
ORIGIN

Query Match 99.2%; Score 1631.4; DB 6; Length 1908;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1635; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 361 GGCATCTCTAAGCCAAATTTGATTAGTCTAAAAAGATATAGATAAGTTATACCT 420  
Oy 421 gtacaaaaaacgtaactgtatataaacatgttatatgtaacgcaagtgat 480  
Db 421 GTACAAAAAACGTAACGTATATAAACCATTTGATATATGACAGCAAGGATATAT 480  
Oy 481 agagttatcaatcactgtaacacttatataaaaaaacctcacaagtttcaagga 540  
Db 481 AGAGTTATCAATTCATGACCAACTTTATTAAAAAAACCTCCACAGGTTCAAGGA 540  
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Db 601 TCGGGTTCACCGGTTGGCCAAAGGTGCACTTACTATGAAATTTGGTCACGCGT 660  
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Db 1621 CTGAGAAGAACCAGTGTCTAAG 1641

RESULT 9  
E12279 1908 bp DNA linear PAT 24-JUN-1998  
LOCUS E12279  
DEFINITION cDNA encoding biotinylated Luciola luciferase.  
ACCESSION E12279  
VERSION E12279.1 GI:3251113  
KEYWORDS JP 1996308578-A/4.  
SOURCE Luciola lateralis.  
ORGANISM Luciola lateralis.  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
Elateriformia; Cantharoidea; Lampyridae; Luciola.  
1 (bases 1 to 1908)  
Tatsumi, H., Fukuda, M., Kikuchi, M. and Koyama, T.,  
BIOTIN FIRE FLY LUCIFERASE, BIOTIN FIRE FLY LUCIFERASE GENE, NEW  
RECOMBINANT DNA, PRODUCTION OF BIOTIN FIRE FLY LUCIFERASE AND  
BIOLUMINESCENCE ANALYSIS  
Patent: JP 1996308578-A 4 26-NOV-1996;  
KIRKMAN CORP  
OS Luciola lateralis  
PN JP 1996308578-A/4  
PD 26-NOV-1996  
PF 24-APR-1995 JP 1995098857  
PR 27-JUL-1994 JP 94P 193798, 14-MAR-1995 JP 95P 54625 PI  
TATSUMI HIROKI, FUKUDA MASARU, KIKUCHI MAMORU, KOYAMA TAJUJI PC  
C12N15/09,C12N9/02,C12Q1/26,(C12N9/02,C12R1:185); CC  
strandedness: Double;  
CC topology: Unknown;  
CC hypothetical: No;  
CC anti-sense: No;  
FH key Location/Qualifiers  
FH  
FT source 1..1908  
FT /clone='pHLf248', /organism='Luciola lateralis' FT  
FT mat\_peptide 1..1908  
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BASE COUNT 598 a 329 c 426 g 555 t  
ORIGIN

Query Match 99.2%; Score 1631.4; DB 6; Length 1908;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1635; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 atggaacaatgtagaagatgaataatgtgtatgtatccctgaaccatttaccatt 60  
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Db 1 ATGGAACAATGAGAGAACGATGAATAATGTGTATGTATGCTCTAACCATTTTTACCTATT 60  
QY 61 gaagaggaatctgtcgtgagacaaatgtgcgaagtatatagatcgatatgcaaaacttga 120  
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Db 61 GAAGAGGAACTCTGCTGAGACAAATGTGCGCAAGTATATGATCGATATGCAAAACTTGA 120  
QY 121 gaattgcttacttaacgacattaccggtgtgtcgtatatacgtgaagccgaatacttga 180  
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Db 121 GCAATTGCTTTTACTAAGCAGCTTACCGGTGTCGATTATACGTACGCCGAACTTAGAA 180  
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Db 181 AAATCATGCGTCTGAGAGAGGCTTTAAAGAAATATGTTGGTTGTTGATGGAAGAAAT 240  
QY 241 gcttattgacgtgaaacttgaagaattcttattctcgttatataagcggattattata 300  
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Db 301 GGTGTGCGTGTGCTCCAACTAATGAGATTATACCTTACGTGAATTGTTCCACAGTTTA 360  
QY 361 ggcattcttaagccaacattgtattagtcttaaaaaagattaaagattataact 420  
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Db 361 GGCATTCTTAAGCCAAACAAATGTATTAGTTCTTAAAAAGAAAGATTAGTAAGTATTACT 420  
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Db 421 GTACAAAAAACGGTAACTGCTATTAAACCATTTGTTATTGGACACAGCAAGTGATTAT 480  
QY 481 agaggtatcaatccatgagcaacttataaaaaaacactccacaagtttcaaga 540  
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Db 481 AGAGGTATCAATCCATGAGCAACTTTATTAATAAAAAACCTCCACAAAGTTTCAAGA 540  
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Db 541 TCAGTTTAAACTGTAGAAAGTTAACCCGAAGAACAAATGCTCTTATAAAGAACTCT 600  
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Db 601 TCGGTTCAACCGGTTTGCCAAAAAGGTGTGCAACTTCTCATGAAATTTGGTACACCGT 660  
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Db 661 TTTTCTCACCGCTAGAGATCCAAATTTATGGAACCAATTTACACAGGCGGCTATTTTTA 720  
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Db 781 GGTTCGTATGTGCAATGTTAAAGAAATTTGACGAAGAGACTTTTAAAAACACTGCAA 840  
QY 841 gattacaatagttcagaagcttattctgtacggaactgtttgcaattcttaagaagt 900  
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Db 841 GATTACAAATGTTCAACCGTTATCTTGTACCAACTTTGTTCCAAATTTTAATAGAAAT 900  
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Db 1021 GGTATAGTTTAAACAGAAACACCTCTGCAATTTATATTCACCCGGAAGCGATGATAAA 1080  
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Db 1081 CCAAGTGTCTTGCGCAAGTGTGCGCAATTTTAAGCAAAAGTTATCGATCTTGATACT 1140  
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Db 1141 AAAAAAATTTGGGCGCCGGAACAGACAGCTGTGGAAGTTGTGTAAGGCTCTATGCTTATG 1200  
QY 1201 aaagttatgttaataatccagaagaacaaaggaatccatagaataaagaggttgggtg 1260  
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Db 1201 AAAGTTATGTATATATCCAGAGCAACAGAGAAATCATATGATGAAGAAAGTGTGTTG 1260

[illegible][illegible][illegible]

Db 961 TTATCTAAGAAATGGTGAAGCTGTGCTAAACGTTTAAATTATCCGGGTTCGTCAA 1020



[illegible]



QY 669 cgctagagatcccaattttaggaacccaagttccaccagcgccgctatttactgtagt 728  
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 QY 729 accatccatcaatggtttgtgtatgttactactttagcctactactgtgtgttttcg 788  
 Db 1104 ACCATTCATCATGTGTTTGGTATGTATTACTTTAGCTATCTAATCTGATGTTTTCG 1163  
 QY 789 tatgtcatgttaacgaaattgacgaagagactttttaaaaaaacctgcgaagatacaa 848  
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 QY 1029 tttaacagaaacaaactctgtcaattatatacacaccggaagcgatgaataacacagtc 1088  
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 QY 1209 tttatgaataatccagaagcaaaagaagaatcatagatgaagaaggttgtgtgcacacag 1268  
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 Db 2004 ACCAGTTGCTAAGATG 2019

RESULT 12  
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 ID E10170 standard: DNA; UNC; 2055 BP.

XX AC E10170:  
 XX SV E10170.1  
 XX DT 08-OCT-1997 (Rel. 52, Created)  
 XX DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)  
 DE DNA encoding mutated streptavidin-firefly luciferase fusion protein.  
 XX KW JP 1995289264-A/2.  
 XX OS unidentified.  
 XX OC unclassified.  
 XX RN [1]  
 RP 1-2055  
 RA Tatsumi H., Fukuda M.;  
 RT "VARIANT TYPE STREPTAVIDIN GENE, FUSION PROTEIN GENE OF VARIANT TYPE  
 STREPTAVIDIN-FIREFLY LUCIFERASE, NEW RECOMBINANT AND PRODUCTION OF FUSION  
 PROTEIN OF VARIANT TYPE STREPTAVIDIN-FIREFLY LUCIFERASE";  
 RL Patent number JP1995289264-A/2, 07-NOV-1995.  
 RL KIKKOMAN CORP.  
 XX OS None  
 CC OC Artificial sequences.  
 CC PN JP 1995289264-A/2  
 CC PD 07-NOV-1995  
 CC PF 27-APR-1994 JP 1994090275  
 CC PI TATSUMI HIROKI, FUKUDA MASARU  
 CC PC C12N15/09, C07K14/36, C07K19/00, C12P21/02, G01N33/53, C12P21/02,  
 CC PC C12R1:19;  
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 CC CC anti-sense: No;  
 CC FH key Location/Qualifiers  
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 Best Local Similarity 99.5%; Pred. No. 0;  
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## RESULT 13

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 DEFINITION Sequence 5 from patent US 5814465.  
 ACCESSION AR043316  
 VERSION AR043316.1 GI:5964324  
 KEYWORDS  
 SOURCE  
 ORGANISM

## REFERENCE

1 (bases 1 to 1704)  
 Tatum, H., Fukuda, S., Kikuchi, M. and Koyama, Y.  
 Biotinized firefly luciferase, a gene for biotinated firefly luciferase, a recombinant DNA, a process for producing biotinated luciferase and a bio-luminescent analysis method  
 Patent: US 5814465-A 5 29-SEP-1996.

## JOURNAL FEATURES

source Location/Qualifiers  
 BASE COUNT 541 a 275 c 361 g 527 t  
 ORIGIN

Query Match 98.7%; Score 1622.8; DB 6; Length 1704;  
 Best Local Similarity 99.6%; Pred. No. 0;  
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ACCESSION	E12278		
VERSION	E12278.1	GI:3251112	
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ORGANISM	Luciola lateralis.		
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AUTHORS	Tatsumi,H., Fukuda,M., Kikuchi,M. and Koyama,T.		
TITLE	BIOTIN FIRE FLY LUCIFERASE, BIOTIN FIRE FLY LUCIFERASE GENE, NEW RECOMBINANT DNA, PRODUCTION OF BIOTIN FIRE FLY LUCIFERASE AND BIOLUMINESCENCE ANALYSIS		
JOURNAL	Patent: JP 1996308578-A 3 26-NOV-1996;		
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PD	26-NOV-1996		
PR	24-APR-1995 JP 1995098857		
PR	27-JUL-1994 JP 94P 193798, 14-MAR-1995 JP 95P 54625 PT		
TATSUMI HIROKI, FUKUDA MASARU, KIKUCHI MAMORU, KOYAMA TAJIJI PC			
C12N15/09,C12N9/02,C12Q1/26,(C12N9/02,C12R1.185); CC			
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CC hypothetical: No;			
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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21: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*  
22: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*  
23: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*  
24: /SIDS5/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1644	100.0	1644	20	AAx84395
2	1640.8	99.8	1644	20	AAx84396
3	1639.2	99.7	1644	20	AAx25718
4	1636	99.5	1644	14	AAQ34745
5	1632.8	99.3	1644	14	AAQ34745
6	1631.4	99.2	1908	18	AAQ3257
7	1631.4	99.2	1920	19	AAV32467
8	1623.2	98.7	2019	17	AAV33850
9	1623.2	98.7	2055	17	AAV33851

10	1622.8	98.7	1704	18	AAV63268
11	1622.8	98.7	1704	19	AAV23595
12	1621.6	98.6	2364	19	AAV23580
13	1493.6	90.9	1556	20	AAx25717
14	1356	82.5	1644	10	AAV91170
15	1356	82.5	1644	11	AAQ03801
16	1356	82.5	1644	12	AAQ13844
17	1356	82.5	1644	22	AAQ92231
18	1356	82.5	1644	24	AAQ22186
19	1354.4	82.4	1644	14	AAQ13825
20	1354.4	82.4	1644	12	AAQ34987
21	1352.8	82.3	1644	12	AAQ13840
22	1352.8	82.3	1644	12	AAQ13841
23	1352.8	82.3	1644	12	AAQ13842
24	1352.8	82.3	1644	12	AAQ13843
25	1352.8	82.3	1644	12	AAQ13845
26	1263.2	76.8	1656	20	AAx25716
27	1040.8	63.3	1656	20	AAx25715
28	1016	61.8	1970	16	AAV00613
29	748.4	45.5	10533	16	AAQ98930
30	748.4	45.5	10558	16	AAQ98912
31	748	45.5	6565	22	AAV55126
32	748	45.5	6971	22	AAV55124
33	748	45.5	7558	22	AAV55125
34	748	45.5	7969	22	AAV55123
35	745.8	45.4	5427	22	AAQ83390
36	745.2	45.3	1811	15	AAQ58732
37	745.2	45.3	5620	18	AAV48630
38	745.2	45.3	5620	22	AAV30233
39	745.2	45.3	5789	20	AAV08779
40	745.2	45.3	5791	20	AAV08778
41	745.2	45.3	5793	20	AAV08776
42	745.2	45.3	5793	20	AAV08777
43	745.2	45.3	5818	21	AAV38352
44	745.2	45.3	5819	20	AAV08775
45	745.2	45.3	5819	20	AAV08774

## ALIGNMENTS

RESULT	ID	AAx84395 standard; DNA; 1644 BP.	ALIGNMENTS
AAx84395	AAx84395		
XX	AAx84395:		
AC	09-SEP-1999 (first entry)		
XX			
XX	L. lateralis luciferase coding sequence.		
DE			
XX			
KW	Luciferase; surfactant-tolerant; firefly; intracellular ATP assay; ss.		
OS	Luciola lateralis.		
XX			
PN	WO9933997-A1.		
XX			
XX	08-JUL-1999.		
PD			
XX			
PF	24-DEC-1998; 98WO-JP05864.		
XX			
PR	26-DEC-1997; 97JP-0361022.		
XX			
PA	(KIKK) KIKKOMAN CORP.		
XX			
XX	Hattori N, Murakami S;		
XX			
DR	WPI: 1999-419109/35.		
XX	P-PDB; AAV22182.		
XX			
PT	Modified luciferase tolerant to surfactants and useful for assay of		
XX	intracellular ATP		

PS Example 2; Page 34-39; 56pp; English.  
 CC This sequence encodes a *Luciola lateralis* luciferase of the invention.  
 CC The protein is a surfactant-tolerant luciferase which is derived from  
 CC firefly luciferase by replacement of the glutamic acid residue at  
 CC position 490 by another amino acid. The luciferase can be used in an  
 CC assay of intracellular ATP in biological samples containing cells, for  
 CC example for establishing the presence of cells, and their quantity, in  
 CC the sample. The method can be applied to foodstuffs, drugs,  
 CC agrochemicals, beverages and environmental samples. The activity of the  
 CC surfactant-tolerant luciferase is not lowered by the presence of high  
 CC concentrations of surfactant and therefore an assay of high accuracy can  
 CC be carried out in a simple manner.  
 CC  
 XX Sequence 1644 BP; 528 A; 261 C; 349 G; 506 T; 0 other;

Query Match 100.0%; Score 1644; DB 20; Length 1644;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggaacacatgagacagatgaataattgtatgctgctgaaccatttcctatt 60  
 DB 1 atggaacacatgagacagatgaataattgtatgctgctgaaccatttcctatt 60  
 QY 61 gaagaggaatctgctggaacacatgacgaatataatgatcgatgcaaaacttga 120  
 DB 61 gaagaggaatctgctggaacacatgacgaatataatgatcgatgcaaaacttga 120  
 QY 121 gcaattgctttacttaacgcaacttcggtgtcgaattacgtaacggaacttagaa 180  
 DB 121 gcaattgctttacttaacgcaacttcggtgtcgaattacgtaacggaacttagaa 180  
 QY 181 aatcaatgctgctgaagagagccttaagaattatgctgtgtttatggaagaatt 240  
 DB 181 aatcaatgctgctgaagagagccttaagaattatgctgtgtttatggaagaatt 240  
 QY 241 gcgttatgcagtgaacactgtgaagaattccttattcctgtatagccggttattata 300  
 DB 241 gcgttatgcagtgaacactgtgaagaattccttattcctgtatagccggttattata 300  
 QY 301 ggtgtcgtgtgtgtcccaactatgatattacacttcacgtgaattgttcaagttta 360  
 DB 301 ggtgtcgtgtgtgtcccaactatgatattacacttcacgtgaattgttcaagttta 360  
 QY 361 ggcattctcaagccaacaaatgtattatgtcttaaaaaaggattagataaagtataact 420  
 DB 361 ggcattctcaagccaacaaatgtattatgtcttaaaaaaggattagataaagtataact 420  
 QY 421 gtacaaaaaagcgttaactgtctataaaccattgttataatggaacgaagtgtgattat 480  
 DB 421 gtacaaaaaagcgttaactgtctataaaccattgttataatggaacgaagtgtgattat 480  
 QY 481 aagagttatcaatcatatggaacacatttataaaaaaacaccaccaagtttcaaga 540  
 DB 481 aagagttatcaatcatatggaacacatttataaaaaaacaccaccaagtttcaaga 540  
 QY 541 tcaagttttaaactgttaagaatttaacccaagaacaagttgtcttataatgaactct 600  
 DB 541 tcaagttttaaactgttaagaatttaacccaagaacaagttgtcttataatgaactct 600  
 QY 601 tgggtttcaacccgtttgccaagaagtgatgaacttaactcaatgaaattgttcaactaga 660  
 DB 601 tgggtttcaacccgtttgccaagaagtgatgaacttaactcaatgaaattgttcaactaga 660  
 QY 661 tttttcagctagagatccaaattatggaacaaagtccacggccggtatttta 720  
 DB 661 tttttcagctagagatccaaattatggaacaaagtccacggccggtatttta 720  
 QY 721 actgtagtaacatccatcatatgattgtgtaagttaactacttaggcataacttgt 780  
 DB 721 actgtagtaacatccatcatatgattgtgtaagttaactacttaggcataacttgt 780

QY 781 ggttcgtatgtcatgttaacgaataattgacgaagagactttttaaacaactgca 840  
 DB 781 ggttcgtatgtcatgttaacgaataattgacgaagagactttttaaacaactgca 840  
 QY 841 gattacaatgttcaagcgttattcttctgtacgcaactgtttgcaattcctaagaagt 900  
 DB 841 gattacaatgttcaagcgttattcttctgtacgcaactgtttgcaattcctaagaagt 900  
 QY 901 gaatttcgtataataatgatttataaatttgaattgaaattcactgtgcaagacct 960  
 DB 901 gaatttcgtataataatgatttataaatttgaattgaaattcactgtgcaagacct 960  
 QY 961 ttacttaagaanaattgtgaagctgtgtgacagcttttaattacgggtgtgtcga 1020  
 DB 961 ttacttaagaanaattgtgaagctgtgtgacagcttttaattacgggtgtgtcga 1020  
 QY 1021 ggtctatgtttaacagaacaacctctgcaattatatacaccggaagcgatgataa 1080  
 DB 1021 ggtctatgtttaacagaacaacctctgcaattatatacaccggaagcgatgataa 1080  
 QY 1081 ccaggtgcttcttgccaagttgtgcatattttaagaacaaagtatcgatctgtact 1140  
 DB 1081 ccaggtgcttcttgccaagttgtgcatattttaagaacaaagtatcgatctgtact 1140  
 QY 1141 aaaaaaacttggcccgacacagacgtggaagattgtgtlaaaggtccatgctatg 1200  
 DB 1141 aaaaaaacttggcccgacacagacgtggaagattgtgtlaaaggtccatgctatg 1200  
 QY 1201 aaagttatgtatgaataccagaagcaacaagaagaatcatagatgaagaagttgtg 1260  
 DB 1201 aaagttatgtatgaataccagaagcaacaagaagaatcatagatgaagaagttgtg 1260  
 QY 1261 cacacagagatattgtgattacagatgaagaagaacatttcttctgtgagctgttg 1320  
 DB 1261 cacacagagatattgtgattacagatgaagaagaacatttcttctgtgagctgttg 1320  
 QY 1321 aagttcttaatacaatacaagaagatalcaagtaaccctgtgtaattagaatctgtctt 1380  
 DB 1321 aagttcttaatacaatacaagaagatalcaagtaaccctgtgtaattagaatctgtctt 1380  
 QY 1381 ttgcaacatcccaaatatttttgaatgcggcggtgtgcgtgtcccaatccataagctgtg 1440  
 DB 1381 ttgcaacatcccaaatatttttgaatgcggcggtgtgcgtgtcccaatccataagctgtg 1440  
 QY 1441 gagcttcgggagcgtgtttgttgaacttaagaagaagaatctatgactgaagaaga 1500  
 DB 1441 gagcttcgggagcgtgtttgttgaacttaagaagaagaatctatgactgaagaaga 1500  
 QY 1501 atggaattacgttgcagtaagttcaaatgcaaaacgittgcgtgtgtgcgtttt 1560  
 DB 1501 atggaattacgttgcagtaagttcaaatgcaaaacgittgcgtgtgtgcgtttt 1560  
 QY 1561 gtggaagaagttaacaaagttcactgttaaatgtaacgtgaagaacattagaagaata 1620  
 DB 1561 gtggaagaagttaacaaagttcactgttaaatgtaacgtgaagaacattagaagaata 1620  
 QY 1621 ctgaagaacacagttgtctaagatg 1644  
 DB 1621 ctgaagaacacagttgtctaagatg 1644

RESULT 2  
 AAX84396  
 ID AAX84396 standard; DNA; 1644 BP.  
 XX  
 AC AAX84396;  
 XX  
 DT 09-SEP-1999 (first entry)  
 XX  
 XX L. lateralis luciferase coding sequence.  
 DE  
 XX Luciferase; surfactant-tolerant; firefly; intracellular ATP assay; ss.  
 XX



OS Luciola lateralis.  
XX MO9933997-A1.  
XX 08-JUL-1999.  
XX 24-DEC-1998; 98WO-JP05864.  
XX 26-DEC-1997; 97JP-0361022.  
XX (KIKK ) KIKKOMAN CORP.  
XX Hattori N, Murakami S;  
XX WPI: 1999-419109/35.  
XX P-PSDB: MAY22183.  
XX Modified luciferase tolerant to surfactants and useful for assay of  
PT intracellular ATP  
XX  
XX Example 2; Page 43-48; 56pp; English.  
XX This sequence encodes a Luciola lateralis luciferase of the invention.  
CC The protein is a surfactant-tolerant luciferase which is derived from  
CC firefly luciferase by replacement of the glutamic acid residue at  
CC position 490 by another amino acid. The luciferase can be used in an  
CC assay of intracellular ATP in biological samples containing cells, for  
CC example for establishing the presence of cells, and their quantity, in  
CC the sample. The method can be applied to foodstuffs, drugs,  
CC agrochemicals, beverages and environmental samples. The activity of the  
CC surfactant-tolerant luciferase is not lowered by the presence of high  
CC concentrations of surfactant and therefore an assay of high accuracy can  
CC be carried out in a simple manner.  
XX  
XX Sequence 1644 BP; 529 A; 262 C; 348 G; 505 T; 0 other;

Query Match 99.8%; Score 1640.8; DB 20; Length 1644;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1642; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atggaacaatggaagacatgtaaaatctgtatggtcctgaacaattaccctatt 60  
DB 1 atggaacaatggaagacatgtaaaatctgtatggtcctgaacaattaccctatt 60  
QY 61 gaagaggatctgctgagcgacaatttgcgaagtatagtcgatacgcaaaacttga 120  
DB 61 gaagaggatctgctgagcgacaatttgcgaagtatagtcgatacgcaaaacttga 120  
QY 121 gcaattgctttacttaacgacattaccggttgcgattatagctacgacgaatactaga 180  
DB 121 gcaattgctttacttaacgacattaccggttgcgattatagctacgacgaatactaga 180  
QY 181 aaatcaatgctgtctagagagagctttaagaattatggttgcgtgtatgtagaagaatt 240  
DB 181 aaatcaatgctgtctagagagagctttaagaattatggttgcgtgtatgtagaagaatt 240  
QY 241 ggttatcgatgaaactgtgaagaattcttattcctgatttagccggtttattata 300  
DB 241 ggttatcgatgaaactgtgaagaattcttattcctgatttagccggtttattata 300  
QY 301 ggttcggtgtgctccacaactaatgattatgattacactcaagtgatggttccacggttta 360  
DB 301 ggttcggtgtgctccacaactaatgattatgattacactcaagtgatggttccacggttta 360  
QY 361 ggcattccttaagccaactatgtattatgcttcttaaaaaagattagataaagtataact 420  
DB 361 ggcattccttaagccaactatgtattatgcttcttaaaaaagattagataaagtataact 420  
QY 421 gtaacaaaaacggtactagctatataaacattgttatattatggaagaaagtgtgatat 480  
DB 421 gtaacaaaaacggtactagctatataaacattgttatattatggaagaaagtgtgatat 480

QY 481 agagttatcatccatggaacaaatttataaaaaaacctccacaaagtttcaaga 540  
DB 481 agagttatcatccatggaacaaatttataaaaaaacctccacaaagtttcaaga 540  
QY 541 tcaagtttaaaactgtagaagtttaacccgaagaacagttgctcttataatgaact 600  
DB 541 tcaagtttaaaactgtagaagtttaacccgaagaacagttgctcttataatgaact 600  
QY 601 tcggttcaacccggtttgcgaagaagtgctcaacttaccatgaataatttgcactaga 660  
DB 601 tcggttcaacccggtttgcgaagaagtgctcaacttaccatgaataatttgcactaga 660  
QY 661 ttcttcacgttagagatccaatltatggaaccaaagtttccacgaagcgactattta 720  
DB 661 ttcttcacgttagagatccaatltatggaaccaaagtttccacgaagcgactattta 720  
QY 721 actgttagaccattccatcgtgttttgcgtatgttttaccatttaagctatcctaatt 780  
DB 721 actgttagaccattccatcgtgttttgcgtatgttttaccatttaagctatcctaatt 780  
QY 781 ggttttcgtatgtcatgttaacgaaatttgacgaagagactttttaaacaactgcga 840  
DB 781 ggttttcgtatgtcatgttaacgaaatttgacgaagagactttttaaacaactgcga 840  
QY 841 gattacaatgttccaaagcttattctgttaccgaacttgttgcaattccttaataaga 900  
DB 841 gattacaatgttccaaagcttattctgttaccgaacttgttgcaattccttaataaga 900  
QY 901 gaattactcgataatattgtttatatacaatttggtaattgcatctgaggagacct 960  
DB 901 gaattactcgataatattgtttatatacaatttggtaattgcatctgaggagacct 960  
QY 961 ttacttaagaagaatttgcgaagctgtgttcagacggttttaccggtgttcgca 1020  
DB 961 ttacttaagaagaatttgcgaagctgtgttcagacggttttaccggtgttcgca 1020  
QY 1021 ggtctatgtttaacagaacaaacctctgcaattatataccacgggaagcgatgataa 1080  
DB 1021 ggtctatgtttaacagaacaaacctctgcaattatataccacgggaagcgatgataa 1080  
QY 1081 ccaggtgcttctcgcaagttgtgcatttttaagaagaaattatcgatctgtgact 1140  
DB 1081 ccaggtgcttctcgcaagttgtgcatttttaagaagaaattatcgatctgtgact 1140  
QY 1141 aaaaaaacttggcccggaacagacgtggaagattgtttaagaagttccatcgctatg 1200  
DB 1141 aaaaaaacttggcccggaacagacgtggaagattgtttaagaagttccatcgctatg 1200  
QY 1201 aaagttatgtagaataccagaagcaacaagaataatcatalagagaaggttggtg 1260  
DB 1201 aaagttatgtagaataccagaagcaacaagaataatcatalagagaaggttggtg 1260  
QY 1261 caccacagagatatgtgttatccgataagaagaataatttcttcgtgagatggtt 1320  
DB 1261 caccacagagatatgtgttatccgataagaagaataatttcttcgtgagatggtt 1320  
QY 1321 aagctttaatcaatacaagaagatcatcaagttaccacctcgtgaattagaatctgttct 1380  
DB 1321 aagctttaatcaatacaagaagatcatcaagttaccacctcgtgaattagaatctgttct 1380  
QY 1381 ttgcaacatccaaatattttgattgctcggtgtgtgcgttccagatccatagctgtg 1440  
DB 1381 ttgcaacatccaaatattttgattgctcggtgtgtgcgttccagatccatagctgtg 1440  
QY 1441 gagcttccggagctgtgtgtgttacttaagaagaagaaatctatgactggaagaagta 1500  
DB 1441 gagcttccggagctgtgtgtgttacttaagaagaagaaatctatgactggaagaagta 1500  
QY 1501 atggttaacgttgcgttagtcaagttccaatgcaaaacggttgcgtgtgttgcgtttt 1560  
DB 1501 atggttaacgttgcgttagtcaagttccaatgcaaaacggttgcgtgtgttgcgtttt 1560  
QY 1561 gtgagcgaagtacctaagaagtlctcatgtgttaaaattgacggtlaaagaacttaga 1620



DB 1261 cacacagagatattggtatctacgataagaacaaacattcttaccgtgacgtttg 1320  
 OY 1321 aagctttaaatacaataaagaagataataacacactgctgaattgaattcgtctt 1380  
 DB 1321 aagctttaaatacaataaagaagataataacacactgctgaattgaattcgtctt 1380  
 OY 1381 ttgcacacccaataatttttgatgcggcgttgcgtgcttccagacccatagctgt 1440  
 DB 1381 ttgcacacccaataatttttgatgcggcgttgcgtgcttccagacccatagctgt 1440  
 OY 1441 gagcttcgggagctgtgtgttgaacttaagaagaagaatactatgactgaagaagta 1500  
 DB 1441 gagcttcgggagctgtgtgttgaacttaagaagaagaatactatgactgaagaagta 1500  
 OY 1501 atggtattcgttgcgtacgaattccaataaagcttgcgtggtggtcgtcttt 1560  
 DB 1501 atggtattcgttgcgtacgaattccaataaagcttgcgtggtggtcgtcttt 1560  
 OY 1561 gtgagcgaagtaacccaagctcactgtaaatgacggttaagaacatagagaata 1620  
 DB 1561 gtgagcgaagtaacccaagctcactgtaaatgacggttaagaacatagagaata 1620  
 OY 1621 ctgaagaacacagctgtcgaagt 1644  
 DB 1621 ctgaagaacacagctgtcgaagt 1644

RESULT 4

AA034745  
 ID AA034745 standard; cDNA to mRNA; 1644 BP.

AC AA034745;

DT 24-MAY-1993 (first entry)

DE Thermostable luciferase (wild-type).

KW Firefly; Luciola cruciata; GENI; Luciola lateralis; HEIKE;

OS mutant; assay; ss.

XX Luciola lateralis.

PN EP524448-A.

PD 27-JAN-1993.

PF 26-JUN-1992; 92EP-0110808.

PR 27-JUN-1991; 91JP-0157117.

PR 29-NOV-1991; 91JP-0317064.

PR 22-MAY-1992; 92JP-0131057.

PA (KIRK) KIRKMAN CORP.

PI Elitchi N, Naoki K;

DR WPI: 1993-028553/04.

DR P-PSDB; AAR30803.

PS Claim 1-3; Page 29-30 + 21-24; 33pp; English.

XX A DNA sequence of a thermostable luciferase of a firefly, which encodes the amino acid sequence of a wild-type firefly luciferase in which an amino acid at the 217 position or an amino acid at the CC position equiv. to the 217 position of the luciferase of Luciola cruciata (GENI firefly) of Luciola lateralis (HEIKE firefly) is replaced by a hydrophobic amino acid, esp. Ile, Leu or Val, is claimed. The mutant luciferase is identical in properties to the

CC wild-type luciferase except that it is stable when heated to high  
 CC temps., e.g. 50 degrees C. The luciferase can be used in assays for  
 CC e.g. ATP.  
 XX  
 SQ Sequence 1644 BP; 529 A; 262 C; 349 G; 504 T; 0 other;

Query Match 99.5%; Score 1636; DB 14; Length 1644;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1639; Conservatve 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 atggaacacatgagagacatggaataatggtatggtcctgaacatttaccatt 60  
 DB 1 atggaacacatgagagacatggaataatggtatggtcctgaacatttaccatt 60  
 OY 61 gaagagagactcgtctgtagacacaaatctgcgaagatataatgataatggaacttga 120  
 DB 61 gaagagagactcgtctgtagacacaaatctgcgaagatataatgataatggaacttga 120  
 OY 121 gcaattccttacttaacacgacatacctacggtgtcgattatacgtacgccaatacttagaa 180  
 DB 121 gcaattccttacttaacacgacatacctacggtgtcgattatacgtacgccaatacttagaa 180  
 OY 181 aaatcatgctgtctagagagagcttaagaataatggttggttgttgatggaagaatt 240  
 DB 181 aaatcatgctgtctagagagagcttaagaataatggttggttgttgatggaagaatt 240  
 OY 241 gcgttatgcagtggaacactggaagaattccttataccgtatattagccggtattata 300  
 DB 241 gcgttatgcagtggaacactggaagaattccttataccgtatattagccggtattata 300  
 OY 301 ggttcgtgtgtggtcccaactaagatatacacttaacgtgaattggttccacagttta 360  
 DB 301 ggttcgtgtgtggtcccaactaagatatacacttaacgtgaattggttccacagttta 360  
 OY 361 ggcactctaaagccaacaaatgtatcttaataaaaggatagataaagtataact 420  
 DB 361 ggcactctaaagccaacaaatgtatcttaataaaaggatagataaagtataact 420  
 OY 421 gtacaaaaaagcgttaacactgctatataaaacactgttatatgagcagaagtgatatt 480  
 DB 421 gtacaaaaaagcgttaacactgctatataaaacactgttatatgagcagaagtgatatt 480  
 OY 481 agaggtatacaatcactgagacacttataaaacacactccacaaggttttcaaga 540  
 DB 481 agaggtatacaatcactgagacacttataaaacacactccacaaggttttcaaga 540  
 OY 541 tcaagttttaaactgttagaagtttaacccgcaagaagttgcttataatgaactc 600  
 DB 541 tcaagttttaaactgttagaagtttaacccgcaagaagttgcttataatgaactc 600  
 OY 601 tccggttcaacccgttttgcgaagaaggtgtgcaacttactcaatgaatgacgtactaga 660  
 DB 601 tccggttcaacccgttttgcgaagaaggtgtgcaacttactcaatgaatgacgtactaga 660  
 OY 661 ttcttcacgcttagagatccaattatagaaacaaagtttccacaggaacggtatttta 720  
 DB 661 ttcttcacgcttagagatccaattatagaaacaaagtttccacaggaacggtatttta 720  
 OY 721 actgtatgacacatccatcatggtttgtgttactacttaagctatcactgtg 780  
 DB 721 actgtatgacacatccatcatggtttgtgttactacttaagctatcactgtg 780  
 OY 781 ggttttgatgtgcatgttgaagaaatctgacgaagactttttaaaacactgcaa 840  
 DB 781 ggttttgatgtgcatgttgaagaaatctgacgaagactttttaaaacactgcaa 840  
 OY 841 gattacaatgltcaagcgttattctgttacagactgtttgcaattcttaataagaagt 900  
 DB 841 gattacaatgltcaagcgttattctgttacagactgtttgcaattcttaataagaagt 900  
 OY 901 gaattaccgataaataatgatttcaatttaagttgaattgcatcggcgagacact 960  
 DB 901 gaattaccgataaataatgatttcaatttaagttgaattgcatcggcgagacact 960

Db 901 gaattactcgaataataatgattatcaaatltagttgaattgcatctgcygagcacct 960  
 Qy 961 ttatctaaagaatttgtaagctgtgtgtaagcgttttaattaccgggtgtcttcaa 1020  
 Db 961 ttatctaaagaatttgtaagctgtgtgtaagcgttttaattaccgggtgtcttcaa 1020  
 Qy 1021 ggcattggtttaacagaacaacctgtcaattatatacacacgggaagcgatgataa 1080  
 Db 1021 ggcattggtttaacagaacaacctgtcaattatatacacacgggaagcgatgataa 1080  
 Qy 1081 ccaggtgtctctggcgaagtgtgtccattatattaagaacaaagtctgacttgact 1140  
 Db 1081 ccaggtgtctctggcgaagtgtgtccattatattaagaacaaagtctgacttgact 1140  
 Qy 1141 aaaaaacttggcccgacagacgttgagaagttgtgtgaagggtcctatgctatg 1200  
 Db 1141 aaaaaacttggcccgacagacgttgagaagttgtgtgaagggtcctatgctatg 1200  
 Qy 1201 aaagggtatgtagataatccagaagaacagaagaatcatagatgaagaagttgttg 1260  
 Db 1201 aaagggtatgtagataatccagaagaacagaagaatcatagatgaagaagttgttg 1260  
 Qy 1261 caccacggagatattggtgattacgaatgaagaaaaacattcttctatcgtagatcgttg 1320  
 Db 1261 caccacggagatattggtgattacgaatgaagaaaaacattcttctatcgtagatcgttg 1320  
 Qy 1321 aagcttctaatcaatacaagaagatatacaccacgtcggaattagaatctgtctt 1380  
 Db 1321 aagcttctaatcaatacaagaagatatacaccacgtcggaattagaatctgtctt 1380  
 Qy 1381 ttgcaaatcaataatattttgtagtcggcggtgtgtgctgtccagatccatagctgtg 1440  
 Db 1381 ttgcaaatcaataatattttgtagtcggcggtgtgtgctgtccagatccatagctgtg 1440  
 Qy 1441 gagcttcgggagcgtgtgttctacttaagaagaagaataatctatgatactgaagaagta 1500  
 Db 1441 gagcttcgggagcgtgtgttctacttaagaagaagaataatctatgatactgaagaagta 1500  
 Qy 1501 atggaattcgtgtgtagtaagaatttcaaaatgcaaaacgtttgcgtgtgtgttcgtctt 1560  
 Db 1501 atggaattcgtgtgtagtaagaatttcaaaatgcaaaacgtttgcgtgtgtgttcgtctt 1560  
 Qy 1561 gtgagcgaagtcctcaaaagtcctcgtgttaaatgtgaacgttaagcaattgagaagaata 1620  
 Db 1561 gtgagcgaagtcctcaaaagtcctcgtgttaaatgtgaacgttaagcaattgagaagaata 1620  
 Qy 1621 ctgaagaacacagttgctaagatg 1644  
 Db 1621 ctgaagaacacagttgctaagatg 1644  
 RESULT 5  
 AA003257  
 ID AA003257 standard; DNA; 1644 BP.  
 XX  
 AC AA003257;  
 DT 22-JUL-1990 (first entry)  
 XX  
 DE Luciola lateralis recombinant Luciferase gene.  
 XX  
 KW Luciferase; enzyme; ATP; plasmid pHL7; firefly; ss.  
 XX  
 OS Luciola lateralis.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..1644  
 FT /\*tag= a  
 FT /product=Luciferase  
 FT /EC\_number=EC-1.13.12.7  
 XX  
 PN EP353464-A.  
 XX

PD 07-FEB-1990.  
 XX  
 PF 30-JUN-1989; 89EP-0111958.  
 XX  
 PR 22-DEC-1988; 88JP-0162402.  
 PR 01-JUL-1988; 88JP-0162402.  
 XX  
 PA (KIKK ) KIKKOMAN CORP.  
 XX  
 PI Tatsumi H, Kaiiyama N, Nakano E;  
 XX  
 DR WPI; 1990-038240/06.  
 DR P-PSDB; AAR03731.  
 XX  
 PT New gene encoding luciferase -  
 PT derived from Luciola lateralis and expressed in and purified  
 PT from Escherichia coli genus cells.  
 XX  
 PS Claim 3; page 24; 43pp; English.  
 XX  
 CC This enzyme is useful for determining ATP levels. It is  
 CC contained in plasmid pHL7.  
 XX  
 SQ Sequence 1644 BP; 529 A; 264 C; 348 G; 503 T; 0 other;  
 Query Match 99.3%; Score 1632.8; DB 11; Length 1644;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1637; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 Qy 1 atggaanaacatgagagacatgaanaatattgtatgtagtctgtaacatttaccctatt 60  
 Db 1 atggaanaacatgagagacatgaanaatattgtatgtagtctgtaacatttaccctatt 60  
 Qy 61 gaagagagatctgctgtagacacatttgcgaatgatatgatacgatatacgaaacttga 120  
 Db 61 gaagagagatctgctgtagacacatttgcgaatgatatgatacgatatacgaaacttga 120  
 Qy 121 gcaattgcttcttaacaaacgacttaccggtgtcgtatgatacgtaacgcaatactaga 180  
 Db 121 gcaattgcttcttaacaaacgacttaccggtgtcgtatgatacgtaacgcaatactaga 180  
 Qy 181 aatcatgctgtctagaggaagccttaagaatlaagttgtgtgtgtatgtaagaat 240  
 Db 181 aatcatgctgtctagaggaagccttaagaatlaagttgtgtgtgtatgtaagaat 240  
 Qy 241 gcggtatgtagtgaagaactgtgaagaattcttattctctgtattagccggttattata 300  
 Db 241 gcggtatgtagtgaagaactgtgaagaattcttattctctgtattagccggttattata 300  
 Qy 301 ggtgtcgtgtgtgtccaaactaagatttaccctcagcgtgaattgttacaagtta 360  
 Db 301 ggtgtcgtgtgtgtgtccaaactaagatttaccctcagcgtgaattgttacaagtta 360  
 Qy 361 ggcactctcaagccaacattgtattttagttctaaanaaggaattagataaagttaact 420  
 Db 361 ggcactctcaagccaacattgtattttagttctaaanaaggaattagataaagttaact 420  
 Qy 421 gtacaaaaaagcgtatgctatataaaccattgttataatgtagacagaagtgattat 480  
 Db 421 gtacaaaaaagcgtatgctatataaaccattgttataatgtagacagaagtgattat 480  
 Qy 481 agaggttatcaatcagtagcaactttttaaaaaaacaccccaaggtttcaagga 540  
 Db 481 agaggttatcaatcagtagcaactttttaaaaaaacaccccaaggtttcaagga 540  
 Qy 541 tcaagtttaaacctgttagaagtttaacgcgaagaacagttgctctataatgaactct 600  
 Db 541 tcaagtttaaacctgttagaagtttaacgcgaagaacagttgctctataatgaactct 600  
 Qy 601 tcgggttcaacccggttgcgaagaaggtgtgcaacttactcatgaaattggtcactaga 660  
 Db 601 tcgggttcaacccggttgcgaagaaggtgtgcaacttactcatgaaattggtcactaga 660

QY	661	ttttctcagcgttagagatcccaatttaiggaacccaagtttccacagacgagtcatttta	720
Db	661	ttttctcctacgcgttagagatcccaattctatggaacccaagtttccacagacgagtcatttta	720
QY	721	actgtatgtaacatctccatcatgattggtttgtgtatgtaattactactttaggcctatctaactgt	780
Db	721	actgtatgtaacatctccatcatgattggtttgtgtatgtaattactactttaggcctatctaactgt	780
QY	781	ggttttcgttatctgcatgtttaacgaaatttgacgaagagactttttaaanaacactgcaa	840
Db	781	ggttttcgttatctgcatgtttaacgaaatttgacgaagagactttttaaanaacactgcaa	840
QY	841	gatttaacaaatgttccaagcgttatctcttgcgaacgacttctgtgcgaattcttaaaagaagt	900
Db	841	gatttaacaaatgttccaagcgttatctcttgcgaacgacttctgtgcgaattcttaaaagaagt	900
QY	901	gaattacatcgataataatgatattatccaatttagttgaattgcatctgtcgcgagcaact	960
Db	901	gaattactcgtataataatgatattatccaatttagttgaattgcatctgtcgcgagcaact	960
QY	961	ttatctaaagaanaattggtgtgaagctgttgcctagaagttttaataccgggtgttcgttcaa	1020
Db	961	ttatctaaagaanaattggtgtgaagctgttgcctagaagttttaataccgggtgttcgttcaa	1020
QY	1021	ggcctatggtttaacgaanaaacactcttgcgaatttatccacacccgggaagcgatgatataa	1080
Db	1021	ggcctatggtttaacgaanaaacactcttgcgaatttatccacacccgggaagcgatgatataa	1080
QY	1081	ccagatgctctctgccaagaagttgtgcacattatttaagcaaaaagtatcatgcattgatact	1140
Db	1081	ccagatgctctctgccaagaagttgtgcacattatttaagcaaaaagtatcatgcattgatact	1140
QY	1141	aaaaaaactttgggcccggaacagacgttgaagaagtttgtgtaaaggtccctatgctatg	1200
Db	1141	aaaaaaactttgggcccggaacagacgttgaagaagtttgtgtaaaggtccctatgctatg	1200
QY	1201	aaaggttatctagaataatccagaagaacaagaagaataatcatatgatagaaagaagttggttg	1260
Db	1201	aaaggttatctagaataatccagaagaacaagaagaataatcatatgatagaaagaagttggttg	1260
QY	1261	cacacagagagatattggtgtatctacgatagagaanaaacattcttatactcgtatgcgtttg	1320
Db	1261	cacacagagagatattggtgtatctacgatagagaanaaacattcttatactcgtatgcgtttg	1320
QY	1321	aagccttaatccaataatcaagaagatactcaagttacacacccgtcggaatttagaatctgttctt	1380
Db	1321	aagccttaatccaataatcaagaagatactcaagttacacacccgtcggaatttagaatctgttctt	1380
QY	1381	tttgcacaatccaataattttttgtatgctgcggcggttgcgtgcgcgttccagatccctatgctggt	1440
Db	1381	tttgcacaatccaataattttttgtatgctgcggcggttgcgtgcgcgttccagatccctatgctggt	1440
QY	1441	gagcttccggagagctgtgttctgtacttaagaagaagaataactatgactgaaanaagaagta	1500
Db	1441	gagcttccggagagctgtgttctgtacttaagaagaagaataactatgactgaaanaagaagta	1500
QY	1501	atgattatcagttgttgaatcaagtttccaatgtcaaaaacggttctcgtgtgtgtgtgcgtttt	1560
Db	1501	atgattatcagttgttgaatcaagtttccaatgtcaaaaacggttctcgtgtgtgtgtgtgcgtttt	1560
QY	1561	gttgagacgaatgacccataaagatctccactgtgtaaatgtgacgtgtaaagcaattagaagaata	1620
Db	1561	gttgagacgaatgacccataaagatctccactgtgtaaatgtgacgtgtaaagcaattagaagaata	1620
QY	1621	cttgaagaanaacagtttgcgtataagtg	1644
Db	1621	cttgaagaanaacagtttgcgtataagtg	1644

XX	AA	ATG3269;	
AC			
XX	20-MAR-1997	(first entry)	
DT			
XX	Gene for firefly luciferase conjugated with 87 aa peptide at 3' end.		
DE			
XX	Fusion protein; firefly; luciola lateralis; luciferase; biotinylation;		
KM	wild type; E.coli; bioluminescence assay; quantification; ligand;		
KM	receptor; ds.		
XX			
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	1..1641	
FT		/*tag= a	
FT		/note= "encodes firefly portion of fusion protein"	
FT	CDS	1642..1647	
FT		/*tag= b	
FT		/note= "sequence encoded by linker used to insert	
FT		sequence encoding biotin peptide to generate	
FT		fusion gene"	
FT	CDS	1648..1908	
FT		/*tag= c	
FT		/note= "encodes biotinylated peptide portion of fusion	
FT		protein"	
XX	JP08308578-A.		
PN			
XX	26-NOV-1996.		
PD			
XX	24-APR-1995;	95JP-0098857.	
XX			
PF	14-MAR-1995;	95JP-0054625.	
XX			
PR	27-JUL-1994;	94JP-0193798.	
XX			
PA	(KIKK ) KIKKOMAN CORP.		
XX			
DR	WPI: 1997-059697/06.		
DR	P-PSDB; AAM12395.		
XX			
PT	Fusion protein comprising firefly luciferase and biotinylated		
PT	peptide - useful in a bio-luminescent analytical method for		
PT	quantifying ligands		
XX			
PS	Example 7; Page 11-12; 13pp; Japanese.		
XX			
CC	This is the nucleotide sequence encoding a novel fusion protein which		
CC	comprises the firefly (luciola lateralis) luciferase protein and an 87		
CC	amino acid biotinylated peptide designated the E.coli biotin carboxy		
CC	carrier protein (BCCP-87). The fusion gene was generated by firstly		
CC	amplifying the sequence encoding the E.coli (BCCP-87) from the E.coli		
CC	genome and inserting the resultant sequence into the 3' end of the		
CC	firefly luciferase gene in plasmid pHLf230. The biotin peptide sequence		
CC	replaces the C-terminal Met residue of the wild type luciferase sequence.		
CC	The plasmid was then introduced into E.coli JM101 for production of the		
CC	fusion protein. The novel protein can be used in bioluminescence assays		
CC	to quantify luciferase ligands which may modulate binding of luciferase		
CC	to its receptor.		
XX			
Sequence	1908 BP; 598 A; 329 C; 426 G; 555 T; 0 other;		

RESULT	6
AAT63269	
ID	AAT63269 standard; DNA; 1908 BP.

Query Match	99.2%	Score 1631.4	DB 18	Length 1908
Best Local Similarity	99.6%	Pred. No. 0		
Matches 1635; Conservative	0	Mismatches 6	Indels 0	Gaps 0
Qy	1	atggaacaactgtgagaacgtatgaataatgttctatgtatgctgcctgaacatttaccctatt	60	
Db	1	atggaacaactgtgagaacgtatgaataatgttctatgtatgctgcctgaacatttaccctatt	60	
Qy	61	gaagagagatctgcttgagacaaatttgcgaagtatatgtatgcatatgtcaaaccttga	120	

Db 61 gaagaggatctgctgagcacaattgcgcaatatagtatcgatatgcaaaacttgga 120  
 QY 121 gcaattgctttaaatacgaactacacggtgtcgatatactgacgcgaatactagaa 180  
 Db 121 gcaattgctttaaatacgaactacacggtgtcgatatactgacgcgaatactagaa 180  
 QY 181 aaatcatgctgtcttaagagagagcttaagaataatggttggctgtgtgaagaaat 240  
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 QY 241 gcttatgcaagtgaacacttgagaatttcttcttccttattatgagcggttattata 300  
 Db 241 gcttatgcaagtgaacacttgagaatttcttcttccttattatgagcggttattata 300  
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 Db 301 ggtgtcggtgtggtcccaataatgagattacactcaactgaatgtgtccagttta 360  
 QY 361 ggcattcttaagccaacaaattgtattagtcttaaaaaagattagataaagtataact 420  
 Db 361 ggcattcttaagccaacaaattgtattagtcttaaaaaagattagataaagtataact 420  
 QY 421 gtacaaaaacggttaactgctatataaacattgttatattgagcgcgaagtgattat 480  
 Db 421 gtacaaaaacggttaactgctatataaacattgttatattgagcgcgaagtgattat 480  
 QY 481 agaggttatcaatcatalggaacaaatttataaaaaaacatccacaaaggtttcaagga 540  
 Db 481 agaggttatcaatcatalggaacaaatttataaaaaaacatccacaaaggtttcaagga 540  
 QY 541 taaagtttaaaactgttaagaatttaacgcgaagaacaaagtgctcttataatgaactc 600  
 Db 541 taaagtttaaaactgttaagaatttaacgcgaagaacaaagtgctcttataatgaactc 600  
 QY 601 tcgggttcaacgggtttgcgaagaagtggtcaacttaccataaataattgtgcactaga 660  
 Db 601 tcgggttcaacgggtttgcgaagaagtggtcaacttaccataaataattgtgcacggcgt 660  
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 Db 661 tttcttcacgctagagatcccaatttataggaaacaaagtttcacacgaagcgcgtattta 720  
 QY 721 actgtatgatacattccatcatatggttggatgtttactactttaggcctatctaactgt 780  
 Db 721 actgtatgatacattccatcatatggttggatgtttactactttaggcctatctaactgt 780  
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 Db 781 ggtttcgtatgttcatgttcaacgaatttgacgaagagagactttttaaaaacgtgcaa 840  
 QY 841 gattacaataatgtcaagcgcttattctgttacgcaacttgtttgcaatttctaataagaat 900  
 Db 841 gattacaataatgtcaagcgcttattctgttacgcaacttgtttgcaatttctaataagaat 900  
 QY 901 gaattactcgaataatataattatcaaatattagttgaattgcatctgacgagacact 960  
 Db 901 gaattactcgaataatataattatcaaatattagttgaattgcatctgacgagacact 960  
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 Db 961 ttatctaaagaataatgttgaagcgtgttgcagagcttttaatttaccgggtgtgtcaca 1020  
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 Db 1021 ggcctatgtgttacaagaaacacactcgtcaattatatacacccggaagcgatgtataa 1080  
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 Db 1081 ccagggtcctctgcaaaagtgttgccattatttaagcaaaagtatacgatcttgatact 1140  
 QY 1141 aaaaaaacttggccgcaacagacgttgagagaagtttgtaaaaggtctctatgtctatg 1200  
 Db 1141 aaaaaaacttggccgcaacagacgttgagagaagtttgtaaaaggtctctatgtctatg 1200

QY 1201 aaagttatgtaataatccagaagcaacaagaanaatcataagataagagaagttgttg 1260  
 Db 1201 aaagttatgtaataatccagaagcaacaagaanaatcataagataagagaagttgttg 1260  
 QY 1261 cacacaagagatatgttgatatacgaatgaagaaacatttcttatacgtgagctgttg 1320  
 Db 1261 cacacaagagatatgttgatatacgaatgaagaaacatttcttatacgtgagctgttg 1320  
 QY 1321 aagcttttaatacaataaagaagatatacgaatccactgtcgaatataagatcgttctc 1380  
 Db 1321 aagcttttaatacaataaagaagatatacgaatccactgtcgaatataagatcgttctc 1380  
 QY 1381 ttgcaacatcaaatatttttgatgacggcggtgtgctgcttcacaagatcagctggt 1440  
 Db 1381 ttgcaacatcaaatatttttgatgacggcggtgtgctgcttcacaagatcagctggt 1440  
 QY 1441 gagcttcgggagcgtgtgtgtacttaagaagaaatctatgactgcaaaaaagaatga 1500  
 Db 1441 gagcttcgggagcgtgtgtgtacttaagaagaaatctatgactgcaaaaaagaatga 1500  
 QY 1501 atgattacgttgtcagtcgaatttcaaatgcaaaaagtttggtgtgtgtgtgtt 1560  
 Db 1501 atgattacgttgtcagtcgaatttcaaatgcaaaaagtttggtgtgtgtgtgtt 1560  
 QY 1561 gtgacgaagtaacataaagttcactcactgtaaaattgacggttaagcaaatlaagaata 1620  
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 QY 1621 ctgaagaataaccagttgctaag 1641  
 Db 1621 ctgaagaataaccagttgctaag 1641  
 RESULT 7  
 AAV32467 standard; DNA; 1920 BP.  
 AC AAV32467;  
 XX  
 DT 10-SEP-1998 (first entry)  
 XX  
 DE Luciferase-lysostaphin fused gene.  
 XX  
 KW Luciferase-lysostaphin fused gene; chimeric; bioluminescence; ds.  
 OS Chimeric - Staphylococcus simulans.  
 OS Chimeric - Luciola lateralis.  
 XX  
 FH Key  
 FT CDS Location/Qualifiers  
 FT 1..1920  
 FT /tag= a  
 FT /product= "Luciferase-lysostaphin fusion protein"  
 FT /note= "Nucleotides 1-1647 encode luciferase  
 protein while nucleotides 1648-1920 encode  
 lysostaphin; CDS does not contain stop codon"  
 PN JP10150991-A.  
 XX  
 PD 09-JUN-1998.  
 XX  
 PF 25-NOV-1996; 96GP-0328042.  
 XX  
 PR 25-NOV-1996; 96GP-0328042.  
 XX  
 PA (KIKK ) KIKKOMAN CORP.  
 XX  
 DR WPI: 1998-379994/33.  
 DR P-PSDB: AAM48856.  
 XX  
 PT New Luciferase-lysostaphin fused protein - useful for  
 XX bioluminescence analysis

PS Disclosure; Pages 6-7; 10pp; Japanese.

CC The invention claims for a luciferase-lyso-staphin fused gene which  
 CC encodes a fused protein in which a peptide part consisting of  
 CC luciferase, from *Luciola lateralis*, is connected to a peptide part  
 CC consisting of lyso-staphin from *Staphylococcus simulans*. The method  
 CC described by the invention can be used to prepare a luciferase-  
 CC lyso-staphin fused protein efficiently. The fused protein is useful  
 CC for bioluminescence analysis.

XX Sequence 1920 BP; 627 A; 310 C; 407 G; 576 T; 0 other;

Query Match 99.2%; Score 1631.4; DB 19; Length 1920;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1635; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 atggaanaacatgagagacatgataatattgtatgtgtcctgaacatttaccctat 60  
 Db 1 atggaanaacatgagagacatgataatattgtatgtgtcctgaacatttaccctat 60  
 Qy 61 gaaaggagatctgtcgtgagacaaattgtgcgaattatgtatgcgtatgcgaacttga 120  
 Db 61 gaaaggagatctgtcgtgagacaaattgtgcgaattatgtatgcgtatgcgaacttga 120  
 Qy 121 gcaattgtcttactaacgcaactaccggtgtcgaattatgcgaactgaagccgaacttaaga 180  
 Db 121 gcaattgtcttactaacgcaactaccggtgtcgaattatgcgaactgaagccgaacttaaga 180  
 Qy 181 aaatcatgtctctagagagagccttaagaattatgtgtgtgtgtatgagaaatt 240  
 Db 181 aaatcatgtctctagagagagccttaagaattatgtgtgtgtgtatgagaaatt 240  
 Qy 241 gggatgatgagagaaacgttgaagaattcttaccgttatgacgggttatatta 300  
 Db 241 gggatgatgagagaaacgttgaagaattcttaccgttatgacgggttatatta 300  
 Qy 301 ggtgtcgtgtgtcgtccaaactaatatagattacactctcgtgaattgttcacagttta 360  
 Db 301 ggtgtcgtgtgtcgtccaaactaatatagattacactctcgtgaattgttcacagttta 360  
 Qy 361 ggcattcttaagccaacaattatattagttcttaaaaaagattagataaagttaact 420  
 Db 361 ggcattcttaagccaacaattatattagttcttaaaaaagattagataaagttaact 420  
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 Qy 601 tccgggttcaacccgtttgccaagaaggtgtgcaacttaccatgaaatttgcgcgct 660  
 Db 601 tccgggttcaacccgtttgccaagaaggtgtgcaacttaccatgaaatttgcgcgct 660  
 Qy 661 ttttctcaacgttagagatccaatttataggaaaacaaagtttaccacggcagcgtatatta 720  
 Db 661 ttttctcaacgttagagatccaatttataggaaaacaaagtttaccacggcagcgtatatta 720  
 Qy 721 actgtatgataccatccatcattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 780  
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 Qy 781 ggttttcgtatgtatgtatgaagaatttgaaggaagactttttaaacaactgaa 840  
 Db 781 ggttttcgtatgtatgtatgaagaatttgaaggaagactttttaaacaactgaa 840

Qy 841 gattacaatgttcaacggttatctgttaccgacttgttgcgaattcttaataagaagt 900  
 Db 841 gattacaatgttcaacggttatctgttaccgacttgttgcgaattcttaataagaagt 900  
 Qy 901 gaattctgataataatgatatttacaatttagtgaattgcatctggcgaagcact 960  
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 Db 1021 ggtatgtttaaacaagaacacacctgtcgaattatlaacacacgggaagcgaatgaata 1080  
 Qy 1081 ccaaggtcttcctgcgaagaagttgtgcattttaaagcaaaagttatcgacttgaact 1140  
 Db 1081 ccaaggtcttcctgcgaagaagttgtgcattttaaagcaaaagttatcgacttgaact 1140  
 Qy 1141 aaaaaaacttggcccgaaacagacgtggaagattgtgtlaaagggttccatgtatg 1200  
 Db 1141 aaaaaaacttggcccgaaacagacgtggaagattgtgtlaaagggttccatgtatg 1200  
 Qy 1201 aaaggtatgtagaataaccagaagcaagaagaaatcaatagatgaagaaggttgggtg 1260  
 Db 1201 aaaggtatgtagaataaccagaagcaagaagaaatcaatagatgaagaaggttgggtg 1260  
 Qy 1261 cacaacagagatatttgggtatccagatgaagaagaataacattcttaccgtgtgact 1320  
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 Qy 1321 aagcctttaaatacaatacaagaagatccaagttacacacctgtgaattagatcgttct 1380  
 Db 1321 aagcctttaaatacaatacaagaagatccaagttacacacctgtgaattagatcgttct 1380  
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# RESULT

8  
 AAT33850  
 ID AAT33850 standard; DNA; 2019 BP.

AC AAT33850;

DT 12-NOV-1996 (first entry)

DE DNA encoding streptavidin/luciferase fusion protein.

KW Streptavidin; luciferase; fusion protein;

KW Streptomyces avidinii; *Luciola lateralis*; firefly;

OS recombinant production; Industry; ds.  
 XX Synthetic.

FH Key Location/Qualifiers  
 FT CDS 1..2019  
 XX /\*tag= a  
 PN JP07289264-A.  
 XX  
 XX  
 PD 07-NOV-1995.  
 XX  
 PF 27-APR-1994; 94UP-0090275.  
 XX  
 PR 27-APR-1994; 94UP-0090275.  
 XX  
 PA (KIKK ) KIKKOMAN CORP.  
 XX  
 DR WPI: 1996-015269/02.  
 DR P-PSDB; AAM04208.  
 XX  
 PT New mutant streptavidin (SA) gene - fused to a firefly luciferase  
 gene, for the recombinant prepn. of a SA-FL fused protein  
 XX  
 PS Example 1; Pages 5-6; 12pp; Japanese.  
 CC  
 CC The present sequence encodes a streptavidin/luciferase fusion  
 CC protein, comprising the Streptomyces avidinii streptavidin gene  
 CC and the Luciola lateralis (firefly) luciferase gene. The fusion  
 CC protein can be prepd. by inserting the recombinant DNA encoding  
 CC it into a Escherichia species microbe, culturing the transformed  
 CC microbe in a medium and collecting the fusion protein from the  
 CC culture. The fusion protein can be used in industry.  
 XX  
 SQ Sequence 2019 BP; 590 A; 412 C; 467 G; 550 T; 0 other;

Query Match 98.7%; Score 1623.2; DB 17; Length 2019;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1628; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 9 catgsgaagcagatgaaataatgtgtatgtgtcctgaacatttaccctatgaagagg 68  
 DB 384 cctcgagaacagatgaaataatgtgtatgtgtcctgaacatttaccctatgaagagg 443  
 QY 69 atctgtgtgagcacaatttgcgcaagtatgtatgtatgacaaacttggagcaattgc 128  
 DB 444 atctgtgtgagcacaatttgcgcaagtatgtatgtatgacaaacttggagcaattgc 503  
 QY 129 tttaactaacgcactacccgtgtcgtatatacgtacgcggaacttaaaatcaatc 188  
 DB 504 tttaactaacgcactacccgtgtcgtatatacgtacgcggaacttaaaatcaatc 563  
 QY 189 cgtctagtagagagccttaagaataatgtgtgtgtgtgtatgtatgaagaattgcgtatg 248  
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 QY 309 tctgtgtccaactaatgagatttacactacgtgaattggttcacagtttaagcattc 368  
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 QY 609 aaccggtttgcgaagaagtgtgcgaacttactatgaanaatttgctactgatttctc 668  
 DB 984 aaccggtttgcgaagaagtgtgcgaacttactatgaanaatttgctactgatttctc 1043  
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 DB 1104 accattccatcattgtttgttacttacttacttacttacttacttacttacttactt 1163  
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 DB 1164 tattgtcatgttaacgaanaatttgcgaagaagactttttaaaaacactgcaagattca 1223  
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 QY 909 cgaataaatatgattatcaaatlttagtgaattgtcactcgtcgagacacttatctaa 968  
 DB 1284 cgaataaatatgattatcaaatlttagtgaattgtcactcgtcgagacacttatctaa 1343  
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 DB 1884 cgttgcgtatgaagtttcaaatgtcaaaagtttgcgtgtgtgtgtgtgtgtgtgtgt 1943  
 QY 1569 agtacctaaaggtctcaacgtgttaaaattgaacgttgaagaacatttagaataactgaaga 1628  
 DB 1944 agtacctaaaggtctcaacgtgttaaaattgaacgttgaagaacatttagaataactgaaga 2003  
 QY 1629 accagttgtctaagatg 1644



|||||

Db 2004 accagttgctaagatg 2019

RESULT 9

AAAT33851

ID AAT33851 standard; DNA: 2055 BP.

AC AAT33851;

XX 12-NOV-1996 (first entry)

XX DNA encoding mutant streptavidin/Luciferase fusion protein.

XX

XX Mutant: streptavidin: luciferase: fusion protein:

XX Streptomyces avidinii; Luciola lateralis; firefly;

XX recombinant production; Industry; ds.

XX

XX Synthetic.

XX

XX Key location/Qualifiers

FT CDS 1..2055 a

FT /tag- a

FT /note- "STOP codon absent"

XX

XX JP07289264-A.

XX

XX 07-NOV-1995.

XX

XX 27-APR-1994; 94JP-0090275.

XX

XX 27-APR-1994; 94JP-0090275.

XX

XX (KIKK ) KIKKOMAN CORP.

XX

XX WPI; 1996-015269/02.

XX P-PSDB; AAM04208.

XX

XX New mutant streptavidin (SA) gene - fused to a firefly luciferase

XX gene, for the recombinant prepn. of a SA-FL fused protein

XX

XX Claim 1; Pages 7-8; 12pp; Japanese.

XX

XX The present sequence encodes a mutant streptavidin/Luciferase

XX fusion protein, comprising a mutant Streptomyces avidinii

XX streptavidin gene and the Luciola lateralis (firefly) luciferase

XX gene. The fusion protein can be prepd. by inserting the

XX recombinant DNA encoding it into a Escherichia species microbe,

XX culturing the transformed microbe in a medium and collecting the

XX fusion protein from the culture. The fusion protein can be used

XX in industry.

XX

XX Sequence 2055 BP; 603 A; 418 C; 474 G; 560 T; 0 other:

XX

Query Match 98.7%; Score 1623.2; DB 17; Length 2055;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1628; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 9 catgagagacatgaaatattgtatgtgctcgaacacatttaccctattgagaagg 68

Db 420 cctcgagagacatgaaatattgtatgtgctcgaacacatttaccctattgagaagg 479

Qy 69 atcgtgtagacacaaatgagacatgatacgatcgatacgaaaacttgagcaattgc 128

Db 480 atctgtagacacaaatgagacatgatacgatcgatacgatacgaaaacttgagcaattgc 539

Qy 129 tttaactaacgacttaccggtgtcgattatcgatcgatcgacgcaacttagaagaatacatg 188

Db 540 tttaactaacgacttaccggtgtcgattatcgatcgatcgacgcaacttagaagaatacatg 599

Qy 189 ctgtctagagagagccttaagaatattggttctgtgtgtatggaagaattggttatg 248

Db 600 ctgtctagagagagccttaagaatattggttctgtgtgtatggaagaattggttatg 659

Qy 249 caatgaaacatgtaagaattcttattctcgttatgaacggttattatagagctgcg 308

Db 660 caatgaaacatgtaagaattcttattctcgttatgaacggttattatagagctgcg 719

Qy 309 tgtgtctccaacttaagaatttaacactcctacgtgaattgtgtcacaagtttaggcactc 368

Db 720 tgtgtctccaacttaagaatttaacactcctacgtgaattgtgtcacaagtttaggcactc 779

Qy 369 taagcacaacattgtatttagtcttaaaaaagattagataagttataactgtcaaaa 428

Db 780 taagcacaacattgtatttagtcttaaaaaagattagataagttataactgtcaaaa 839

Qy 429 aacggttaactgtctattaaacattgttattatggaacgaagtgattatagaagttta 488

Db 840 aacggttaactgtctattaaacattgttattatggaacgaagtgattatagaagttta 899

Qy 489 tcaatccatggaacacttatttaaaaaaacactccacaagtttccaagaagttcaagtt 548

Db 900 tcaatccatggaacacttatttaaaaaaacactccacaagtttccaagaagttcaagtt 959

Qy 549 taaactgttagaagtttaacccgaagaagaagttgtcttataatgaactcttggttc 608

Db 960 taaactgttagaagtttaacccgaagaagaagttgtcttataatgaactcttggttc 1019

Qy 609 aaccggttggccaaaaggtgtgcaacttaactcaatgaagaatttgcatactttctca 668

Db 1020 aaccggttggccaaaaggtgtgcaacttaactcaatgaagaatttgcatactttctca 1079

Qy 669 cgtctagagatcccaattatggaagaaccaagtttccacgaagcagcgtattttaactgtag 728

Db 1080 cgtctagagatcccaattatggaagaaccaagtttccacgaagcagcgtattttaactgtag 1139

Qy 729 accattccatcagtggtttgtatgtttactacttaaggctatcacttggtgttttg 788

Db 1140 accattccatcagtggtttgtatgtttactacttaaggctatcacttggtgttttg 1199

Qy 789 tatgtcatgttgaacgaatttgaacgaagaagactttttaaaaaacactgcaagattaca 848

Db 1200 tatgtcatgttgaacgaatttgaacgaagaagactttttaaaaaacactgcaagattaca 1259

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Db 1260 atgtccaagcttattctctgttaccgaacttgtttgcaattcttaataagaagttaact 1319

Qy 909 cgataaataatgatttacaatttagtgaattgcactgtgagcgacacttatactaa 968

Db 1320 cgataaataatgatttacaatttagtgaattgcactgtgagcgacacttatactaa 1379

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Qy 1029 tttaacagaacaaacctctgcaatttattacacacgggaagcgatgataaacaagttgc 1088

Db 1440 tttaacagaacaaacctctgcaatttattacacacgggaagcgatgataaacaagttgc 1499

Qy 1089 ttctgcaaaagtgtgacattttaaagcaaaagtatcgcacttgataactaaaaaac 1148

Db 1500 ttctgcaaaagtgtgacattttaaagcaaaagtatcgcacttgataactaaaaaac 1559

Qy 1149 ttggggccgaacagaagtgagaaagttgttgaaggggtccatgcttatgaaagttta 1208

Db 1560 ttggggccgaacagaagtgagaaagttgttgaaggggtccatgcttatgaaagttta 1619

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Db 1620 tgtagataatccagaagcaagaagaatcatagatgaaaggttggttgacacag 1679

Qy 1269 agatattgggtattcagatgaaagaaaaactcttatacgtgtgactgttgaagcttt 1328

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QY	1031	taacagaacaacacctctgcattatatacacaccggaagcgagataaaccaggttgctt	1090
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QY	1211	tagatataccgaagcaacagaagaatactagaataaaaagttgtgttcacacaagag	1270
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XX
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XX
XX      09-JAN-1996; 96JP-0001812.
XX
XX      09-JAN-1996; 96JP-0001812.
XX
XX      (KIRK ) KIRKMAN CORP.
XX
XX      WPI; 1998-275089/25.
XX      DR
XX      P-PSDB; AAM53883.
XX
XX      Antibody-firefly Luciferase fused protein - and related products
PT      1.e. firefly Luciferase fused gene, recombinant DNA and its
PT      preparation
XX
XX
XX      Disclosure; Page 10-11; 17pp; Japanese.
XX
XX
XX      This sequence encodes a fusion protein of the invention. The protein is
CC      a antibody-firefly Luciferase fusion protein, in which an antibody part
CC      consisting of a peptide having antibody activity is combined with an
CC      enzyme part consisting of firefly Luciferase.
XX
XX      Sequence 1704 BP; 541 A; 275 C; 361 G; 527 T; 0 other;
SQ

```

Sequence 1704 BP; 541 A; 275 C; 361 G; 527 T; 0 other;

Query Match	98.78;	Score 1622.8;	DB 19;	Length 1704;
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Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1627; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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wy

Db 71 tcgagaacgcatgaaatatgtgtatgtcctgaacatttaccctattgaaggat 130

Ov 71 ctactgaacacaaattgcgcaatataatgaatcaatatcaaaaaacttgaagcaattgctt 130

[illegible]

Db 131 ctgctgagcacaattgcgcaagtatatgtatcgatatgcaaaacttgagcgaattgctt 190

131 ttactaacqcaacttaaccqqtgttcgattatatacgtacgcgcgaataacttagaaaaaatcatgct 190

Db 191 ttactaacgcacttaaccggtgtcgaatlacgtacgcgcgaalacclagaaaaalcalgc 250

QY 191 gtctagagagagctttaagaattatggtttgtgtgtatggaagaattgcgttatgca 250

[illegible]

BD 231 gCcaGgagagGcLcLaagaaLcLaGg LcGg LcGcLcGaGgaaGgGcLcLaGgaa 220

OY 251 gtgaactgtgaagaattcttattcctgtattagccggttattatagtgctcgtg 310

nb 311 atgaacctatgaaagaattcttattccgataattacccgaattattataaqtatcgaqtg 370

[illegible]

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CCTT TTTT CCCC A30

3/1 agcccaacaaatctgcatccttagtctcctaataaggaactagaacaagtccaacatgcaccacaaaat +30

Db 431 agccaacattgtatttagttcctaaaaagattagataagttataactgtacaaaaa 490

431 cctaacctcctat+aaaaaccat+attatat+gaacacgaaatgaattataagaattatc 490

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491 aatccatggaactttatataaaaaaacactccacaaqtttcaaaqatcaagtltta 550

Db 551 aatccatgacaactttatataaaaaaacactccacaaggtttcaaggtatcaagttlta 610

QY 551 aaactgtagaagtttaaccgcaagaacaagttgtctctataatgaactcttcggttcaa 610

670

Dd bll aaactgtagaagtcataccgcgaagaacaaagcgcctcctatcaatgaaccctccggycctcaa o/v

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QY 611 ccggtttgccaagaagtgtgcaacttactcatgaataattgtgloactagattttccagc 670  
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 QY 1271 atattggtatatacgaatgaagaacaaacattcttctacgctgacgcttgaactcttaa 1330  
 |||||||  
 Db 1331 atattggtatatacgaatgaagaacaaacattcttctacgctgacgcttgaactcttaa 1390  
 QY 1331 tcaataacaaagataatacgaatcacactgctgaattagaatctgttctttgcaacatc 1390  
 |||||||  
 Db 1391 tcaataacaaagataatacgaatcacactgctgaattagaatctgttctttgcaacatc 1450  
 QY 1391 caaataattttgatgcggcgctgtgctgagctccagatccatagctgtgagctcccg 1450  
 |||||||  
 Db 1451 caaataattttgatgcggcgctgtgctgagctccagatccatagctgtgagctcccg 1510  
 QY 1451 gagctgtgttcttacttaagaagaanaatctatgactgaaaaaagaagcaatgagattacg 1510  
 |||||||  
 Db 1511 gagctgtgttcttacttaagaagaanaatctatgactgaaaaaagaagcaatgagattacg 1570  
 QY 1511 ttgctagttcaagttccaatgcaaaacgtttgcgtgtgtgtgcgttttctgtgacgaag 1570  
 |||||||  
 Db 1571 ttgctagttcaagttccaatgcaaaacgtttgcgtgtgtgtgtgcgttttctgtgacgaag 1630  
 QY 1571 taacctaaagttctcactgtgtaaatgtgacgttaagcaatttagagaataactgaaagaac 1630  
 |||||||  
 Db 1631 taacctaaagttctcactgtgtaaatgtgacgttaagcaatttagagaataactgaaagaac 1690  
 QY 1631 cagttgctaagaatg 1644  
 |||||||  
 Db 1691 cagttgctaagaatg 1704

RESULT 12  
 AAV23580  
 ID AAV23580 standard; cDNA to mRNA; 2364 BP.  
 XX  
 AC AAV23580;  
 XX  
 DT 16-JUL-1998 (first entry)  
 XX  
 DE Antibody-Firefly luciferase fusion protein gene.  
 KW Firefly luciferase; antibody-luciferase fusion protein; ds.  
 OS Luciola cruciata.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2364  
 FT /tag= a  
 FT /transl\_except= (pos: 670..672, aa: Glu)  
 FT /transl\_except= (pos: 739..741, aa: Trp)  
 FT /transl\_except= (pos: 1369..1371, aa: Ala)  
 FT /note= "no stop codon given"  
 PN JP09187281-A.  
 XX  
 PD 22-JUL-1997.  
 XX  
 PF 09-JUN-1996; 96JP-0001812.  
 PR 09-JUN-1996; 96JP-0001812.  
 PA (KIKK ) KIRKOMAN CORP.  
 XX  
 DR WPI: 1998-275089/25.  
 DR P-PDB; AAM53882.  
 PT Antibody-firefly luciferase fused protein - and related products  
 PT 1.e. firefly luciferase fused gene, recombinant DNA and its  
 PT preparation  
 PS Disclosure: Page 13; 17pp; Japanese.  
 CC This sequence encodes the fusion protein of the invention. The protein is  
 CC a antibody-firefly luciferase fusion protein, in which an antibody part  
 CC consisting of a peptide having antibody activity is combined with an  
 CC enzyme part consisting of firefly luciferase.  
 XX  
 SQ Sequence 2364 BP; 697 A; 444 C; 559 G; 664 T; 0 other;  
 Query Match 98.6%; Score 1621.6; DB 19; Length 2364;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 1627; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
 QY 9 catgagaacgatgataaataatgtgtatgtgtcctgacacatttaccattgaagaagg 68  
 |||||||  
 Db 729 cctcgagaacgatgataaataatgtgtatgtgtcctgacacatttaccattgaagaagg 788  
 QY 69 atctgtgtgagacaaatttgcgaagtatgatgatgataatgcaaaacttggagaatttc 128  
 |||||||  
 Db 789 atctgtgtgagacaaatttgcgaagtatgatgatgataatgcaaaacttggagaatttc 848  
 QY 129 ttctactaacgcaactacccggtgtcgatatacgtacgcgcgaatacttagaataacatcg 188  
 |||||||  
 Db 849 ttctactaacgcaactacccggtgtcgatatacgtacgcgcgaatacttagaataacatcg 908  
 QY 189 ctgtctagaagaaggcttlaaagaatatagtttgtgtgtgtatggaagaatttgcgttatg 248  
 |||||||  
 Db 909 ctgtctagaagaaggcttlaaagaatatagtttgtgtgtgtatggaagaatttgcgttatg 968  
 QY 249 cagtgaacactgtgaagaattcttatctccgtatataccgcggtttattataggtgtcgg 308  
 |||||||  
 Db 969 cagtgaacactgtgaagaattcttatctccgtatataccgcggtttattataggtgtcgg 1028

QY 309 tttgttcccaataatgagatttaactctacgtgaattgttccaggttaaggcatctc 368  
 Db 1029 tttgttcccaataatgagatttaactctacgtgaattgttccaggttaaggcatctc 1088  
 QY 369 taagcacaacattgtattttagttcttaaaaaagattagataaatttaactgtacaaa 428  
 Db 1089 taagcacaacattgtattttagttcttaaaaaagattagataaatttaactgtacaaa 1148  
 QY 429 aacggttaactgtatataaacattgtatatttgagacagaagtgtatagaagttta 488  
 Db 1149 aacggttaactgtatataaacattgtatatttgagacagaagtgtatagaagttta 1208  
 QY 489 tcaatccatggaacattatataaaaaaacatccacagaagtttcaagaatcaagtt 548  
 Db 1209 tcaatccatggaacattatataaaaaaacatccacagaagtttcaagaatcaagtt 1268  
 QY 549 taaaactgtagaagttaacccgcaagaagttgtctcttaataatgaactctcggttc 608  
 Db 1269 taaaactgtagaagttaacccgcaagaagttgtctcttaataatgaactctcggttc 1328  
 QY 609 aacgggttgcacaaagggtgtgcacacttaactcaatgaatattgtcactagatttccca 668  
 Db 1329 aacgggttgcacaaagggtgtgcacacttaactcaatgaatattgtcactagatttccca 1388  
 QY 669 cgttagagatccaatttttggaacaaagtttccacagacggtattttaactgtagt 728  
 Db 1389 cgttagagatccaatttttggaacaaagtttccacagacggtattttaactgtagt 1448  
 QY 729 accattccatcattgttctgtatgttactacttaagcttaactcaactgtgtctcg 788  
 Db 1449 accattccatcattgttctgtatgttactacttaagcttaactcaactgtgtctcg 1508  
 QY 789 tattgtcatgttaacgaatatttgacgaagagactttttaaaaaacactgcgaattaca 848  
 Db 1509 tattgtcatgttaacgaatatttgacgaagagactttttaaaaaacactgcgaattaca 1568  
 QY 849 atgttcaacgcttattctgtacacactgttgcacatttcaataagaagttact 908  
 Db 1569 atgttcaacgcttattctgtacacactgttgcacatttcaataagaagttact 1628  
 QY 909 cgataaataatgattatcaaatattagttgaattgacatgcgcgagacatttactaa 968  
 Db 1629 cgataaataatgattatcaaatattagttgaattgacatgcgcgagacatttactaa 1688  
 QY 969 agaaattgttgaagctgttgcacagcttttaattacccgggtgttcgtcaagctatag 1028  
 Db 1689 agaaattgttgaagctgttgcacagcttttaattacccgggtgttcgtcaagctatag 1748  
 QY 1029 ttttaacagaacaaactctgcacattatatacacccggaagcgatgaataacccaggtgc 1088  
 Db 1749 ttttaacagaacaaactctgcacattatatacacccggaagcgatgaataacccaggtgc 1808  
 QY 1089 ttctggcaaaagtgtgcacattatataagaacaaagtltacgtcttgatcttaaaaaaac 1148  
 Db 1809 ttctggcaaaagtgtgcacattatataagaacaaagtltacgtcttgatcttaaaaaaac 1868  
 QY 1149 ttgtggcccggaacagagtggaagttgttgaagggttctatagcttataagaagttta 1208  
 Db 1869 ttgtggcccggaacagagtggaagttgttgaagggttctatagcttataagaagttta 1928  
 QY 1209 tttgaagtaatccagaagcaacagaagaatctatagagaaggttgggttcacacag 1268  
 Db 1929 tttgaagtaatccagaagcaacagaagaatctatagagaaggttgggttcacacag 1988  
 QY 1269 agatattgtgtattacgatgaagaanaaacattcttactcgttgatcgtttgaagcttt 1328  
 Db 1989 agatattgtgtattacgatgaagaanaaacattcttactcgttgatcgtttgaagcttt 2048  
 QY 1329 aatcaataaagaagatatacaagttaccactgtgaatagaatcgttcttttcacaa 1388  
 Db 2049 aatcaataaagaagatatacaagttaccactgtgaatagaatcgttcttttcacaa 2108

QY 1389 tccaatatttttgatgcgcgctgtgcgttccagatcctatagctgtgtgacttcc 1448  
 Db 2109 tccaatatttttttgatgcgcgctgtgcgttccagatcctatagctgtgtgacttcc 2168  
 QY 1449 gggagctgtgtgtgtacttaagaagaatctatagactgtgaaagaagtaagtata 1508  
 Db 2169 gggagctgtgtgtgtacttaagaagaatctatagactgtgaaagaagtaagtata 2228  
 QY 1509 cgttgcagtcgaagttccaatgcgaacagtttgcgtgtgtgtgtgtgtgtgtgtgt 1568  
 Db 2229 cgttgcagtcgaagttccaatgcgaacagtttgcgtgtgtgtgtgtgtgtgtgtgt 2288  
 QY 1569 agtacctaaggtctcactgtgtaaatgtgacgggtlaaagcaattagaagaatactgaaga 1628  
 Db 2289 agtacctaaggtctcactgtgtaaatgtgacgggtlaaagcaattagaagaatactgaaga 2348  
 QY 1629 accagttgtcgaagatg 1644  
 Db 2349 accagttgtcgaagatg 2364

RESULT 13

AXX25717  
ID AXX25717 standard; cDNA to mRNA, 1656 BP.

AXX25717;

21-MAY-1999 (first entry)

Firefly Luciferase gene #3.

Bioluminescent protein: catalytic efficiency; stability: firefly;

Luciferase; chimeric: luciola cruciata; luciola lateralis;

Photinus pyralis; primer: PCR; amplification; ss.

Chimeric - Luciola lateralis.

Chimeric - Photinus pyralis.

MO9902697-A1.

21-JAN-1999.

30-JUN-1998; 98MO-JP02936.

08-JUL-1997; 97US-0051917.

(KIKK) KIKKOMAN CORP.

Hirokawa K, Kajiyama N, Murakami S;

WPI: 1999-120898/10.

P-PSDB: AAW93366.

New bioluminescent protein with improved properties - has greater

catalytic efficiency and stability and is obtained by modification

of natural precursors

Example 3; Page 30-31; 53pp; Japanese.

The invention relates to the generation of bioluminescent proteins with

improved catalytic efficiency and stability. The proteins are generated

by addition, deletion or substitution of amino acids from a precursor

protein e.g. firefly luciferases, or by constructing chimeric luciferase

proteins from luciferase genes from e.g. Luciola cruciata, L. lateralis

and photinus pyralis. This sequence represents an example of a chimeric

luciferase gene of the invention.

Sequence 1656 BP; 529 A; 283 C; 366 G; 478 T; 0 other;

Query Match 90.9%; Score 1493.6; DB 20; Length 1656;

Best Local Similarity 94.8%; Pred. No. 0; Mismatches 84; Indels 0; Gaps 0;

Matches 1544; Conservative 0;

QY 1 atggaatacctggagaacga tgaataatgtgtatgtctcgaaccatttaccatt 60  
 Db 1 atggaatacctggagaacga tgaataatgtgtatgtctcgaaccatttaccatt 60  
 QY 61 gaagagagatctctgagacacaatttgcgaagtataatgatcgatatgcaaaacttga 120  
 Db 61 gaagagagatctctgagacacaatttgcgaagtataatgatcgatatgcaaaacttga 120  
 QY 121 gcaattgcttactaagcacttaccggtgtcgattatcgtaagcgcgaattacttga 180  
 Db 121 gcaattgcttactaagcacttaccggtgtcgattatcgtaagcgcgaattacttga 180  
 QY 181 aaatcgtctctaggaagagcgtttaaagaattatgttgttctgttga tgaagaatt 240  
 Db 181 aaatcgtctctaggaagagcgtttaaagaattatgttgttctgttga tgaagaatt 240  
 QY 241 gcgttatgcgtgtaaaactgttgaagaattcttaccgttatagccggattattata 300  
 Db 241 gcgttatgcgtgtaaaactgttgaagaattcttaccgttatagccggattattata 300  
 QY 301 ggtgtcgtgtgtgcctcaactaattgaatttacccttgaattgaattgttgcgaatt 360  
 Db 301 ggtgtcgtgtgtgcctcaactaattgaatttacccttgaattgaattgttgcgaatt 360  
 QY 361 ggcattcttaagccacaacttgtatttgaatttctaaaaaagatagaataagtataact 420  
 Db 361 ggcattcttaagccacaacttgtatttgaatttctaaaaaagatagaataagtataact 420  
 QY 421 gtacaaaaaaacggttaactctgtatataaaacatttgaatatttgaacgaagaattgat 480  
 Db 421 gtacaaaaaaacggttaactctgtatataaaacatttgaatatttgaacgaagaattgat 480  
 QY 481 agaggttacaactcgaatgtgcaacttattataaaaaaacctcacaaggtttcaaaaga 540  
 Db 481 agaggttacaactcgaatgtgcaacttattataaaaaaacctcacaaggtttcaaaaga 540  
 QY 541 tcaagttttaaactgttagaagttaacgcgaagaacaaagttgctctataatgaactct 600  
 Db 541 tcaagttttaaactgttagaagttaacgcgaagaacaaagttgctctataatgaactct 600  
 QY 601 tcgggttcaacgcggttgcgaagaaggtgtgcaacttaccatgaataatttgcactaga 660  
 Db 601 tcgggttcaacgcggttgcgaagaaggtgtgcaacttaccatgaataatttgcactaga 660  
 QY 661 ttctccacgctagagatccaatttattggaaccaaagtttcaccagaagcgcatttata 720  
 Db 661 ttctccacgctagagatccaatttattggaaccaaagtttcaccagaagcgcatttata 720  
 QY 721 actgtatgaaccattcgaatcgaatgttggatagtgttactactttagctataacttgg 780  
 Db 721 actgtatgaaccattcgaatcgaatgttggatagtgttactactttagctataacttgg 780  
 QY 781 ggtttcgtatgtcactgttgaagaatttgaacgaagaactttttaaacaactgcaa 840  
 Db 781 ggtttcgtatgtcactgttgaagaatttgaacgaagaactttttaaacaactgcaa 840  
 QY 841 gattacaactgttcaagcgttattctgtacgcgacttggcgaatttcttaataagaagt 900  
 Db 841 gattacaactgttcaagcgttattctgtacgcgacttggcgaatttcttaataagaagt 900  
 QY 901 gaattactcgaataatataatattatcaaatltagtgaattgcatctgscgagaact 960  
 Db 901 gaattactcgaataatataatattatcaaatltagtgaattgcatctgscgagaact 960  
 QY 961 ttactcaagaagaattgtgaagaactgtgtgaagcgttttaatttcaacggtgtgtcgtcaa 1020  
 Db 961 ttactcaagaagaattgtgaagaactgtgtgaagcgttttaatttcaacggtgtgtcgtcaa 1020  
 QY 1021 ggcatagtgttacaagaacacctcgtcaattatatacacccggaagcgatgtataa 1080  
 Db 1021 ggcatagtgttacaagaacacctcgtcaattatatacacccggaagcgatgtataa 1080

QY 1081 ccaagtgctctgcgaagaagttgtgccaattttaaagcaaaagttacatcttgatct 1140  
 Db 1081 ccaagtgctctgcgaagaagttgtgccaattttaaagcaaaagttacatcttgatct 1140  
 QY 1141 aaaaaaacttggcccgcaacagacgttggagaagttgtgtlaaagggtctcatgtatg 1200  
 Db 1141 aaaaaaacttggcccgcaacagacgttggagaagttgtgtlaaagggtctcatgtatg 1200  
 QY 1201 aaaggttatgtagaataatccaagaagcacaagaagaattcaatagaatgaagaagttgt 1260  
 Db 1201 aaaggttatgtagaataatccaagaagcacaagaagaattcaatagaatgaagaagttgt 1260  
 QY 1261 cacaacagagatatgttggtatlaacgatgaagaacaaatttcttatacgtgcatgttg 1320  
 Db 1261 cacaacagagatatgttggtatlaacgatgaagaacaaatttcttatacgtgcatgttg 1320  
 QY 1321 aagttcttaatacaatacaagaagatatacaagtlacacacgtcgtgaattagaattcgtct 1380  
 Db 1321 aagttcttaatacaatacaagaagatatacaagtlacacacgtcgtgaattagaattcgtct 1380  
 QY 1381 ttgcaatcccaaatattttttagtcgcggtgtgtgtgcttccagatctatagctgt 1440  
 Db 1381 ttgcaatcccaaatattttttagtcgcggtgtgtgtgcttccagatctatagctgt 1440  
 QY 1441 gaacttcgggaagcgtgtgtgtgtacttaagaagaacaaatttgaactgaagaagaatga 1500  
 Db 1441 gaacttcgggaagcgtgtgtgtgtacttaagaagaacaaatttgaactgaagaagaatga 1500  
 QY 1501 atgattatcgt 1560  
 Db 1501 atgattatcgt 1560  
 QY 1561 gtggaagaagttacctaagaagttcgaactgtgaataatttgaacgttaagaagaata 1620  
 Db 1561 gtggaagaagttacctaagaagttcgaactgtgaataatttgaacgttaagaagaata 1620  
 QY 1621 ctgaagaa 1628  
 Db 1621 ctcatataa 1628

RESULT 14  
 AAN91170  
 ID AAN91170 standard; DNA; 1644 BP.  
 XX  
 AC AAN91170;  
 DT 14-JUN-1990 (first entry)  
 XX  
 DE Recombinant luciferase gene.  
 XX  
 KW Luciferase; ATP assay; ss.  
 OS Luciola cruciata.  
 XX  
 PN EP301541-A.  
 XX  
 PD 01-FEB-1989.  
 XX  
 PF 28-JUL-1988; 88EP-0112233.  
 XX  
 PR 29-JUL-1987; 87JP-0187724.  
 PR 29-JUL-1987; 87JP-0187725.  
 PR 20-AUG-1987; 87JP-0205194.  
 XX  
 PA (KIKK) KIKKOMAN CORP.  
 PI Masuda T, Tatsumi H, Nakano E;  
 XX  
 DR WPI: 1989-033443/05.  
 DR P-PSDB: AAP94367.  
 XX  
 PT Recombinant luciferase gene - used for efficiently producing luciferase

in E. coli, obtaining a stable and highly active prod.  
 Claim 2: fig 3; 35pp; English.

The sequence was obtd. from cDNA prep'd. from mRNA isolated from  
 L. cruciata tails. The DNA can be incorporated into vectors for  
 transformation of E. coli JM 1010.

Sequence 1644 BP; 529 A; 276 C; 338 G; 501 T; 0 other;

Query Match 82.5%; Score 1356; DB 10; Length 1644;  
 Best Local Similarity 89.1%; Pred. No. 0;  
 Matches 1464; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

1 atcgaaacatgagagacatgaaatattgtgtatgctcgtgaaccatttccatt 60  
 1 atcgaaacatgagagacatgaaatattgtgtatgctcgtgaaccatttccatt 60  
 61 gaagagggatctgtcgtgagacaaatgcycaaglatatgatacgatacgaaacttga 120  
 61 gaagagggatctgtcgtgagacaaatgcycaaglatatgatacgatacgaaacttga 120  
 121 gaattgctttactaactgacacttaccggtgtcogattatacgtacgcgaatttaga 180  
 121 gaattgctttactaactgacacttaccggtgtcogattatacgtacgcgaatttaga 180  
 181 aaatcatgctgtcgtgagagagctttaaagaattatggtttgtttatgagaagaatt 240  
 181 aaatcatgctgtcgtgagagagctttaaagaattatggtttgtttatgagaagaatt 240  
 241 gcgttatgcagtgaanaactgtgaagaatcttattcctgtatagcggattattata 300  
 241 gcgttatgcagtgaanaactgtgaagaatcttattcctgtatagcggattattata 300  
 301 ggttcggtgtgtgcccactaataatgattacactcctcgtgaattgtgttcaagttta 360  
 301 ggttcggtgtgtgcccactaataatgattacactcctcgtgaattgtgttcaagttta 360  
 361 ggcattcctaagcaacaattgtatttatttcttaaaaaaggaattagataaagttaact 420  
 361 ggcattcctaagcaacaattgtatttatttcttaaaaaaggaattagataaagttaact 420  
 421 gtaacaaaaacggttaactgttaaaacattgtatatacttgacagcaaatgtatata 480  
 421 gtaacaaaaacggttaactgttaaaacattgtatatacttgacagcaaatgtatata 480  
 481 agaggttatcaatccatgagacactttatataaaaaaacacccacaagtttcaagta 540  
 481 agaggttatcaatccatgagacactttatataaaaaaacacccacaagtttcaagta 540  
 541 tcaagttttaaactgtgaagtttaacgcgaagaacaagttgtcctttaaataaactct 600  
 541 tcaagttttaaactgtgaagtttaacgcgaagaacaagttgtcctttaaataaactct 600  
 601 tcgggttcaaacggttgcgcaaaagtgtygcaacttactcatcagaataatttgctactaga 660  
 601 tcgggttcaaacggttgcgcaaaagtgtygcaacttactcatcagaataatttgctactaga 660  
 661 ttcttcacgctagaagatccaatttatatgaaaacaaagtttcaacgcgctatatta 720  
 661 ttcttcacgctagaagatccaatttatatgaaaacaaagtttcaacgcgctatatta 720  
 721 actgtagtaccatccatcatgtgtttgtgatacttactacttgagcactatgtg 780  
 721 actgtagtaccatccatcatgtgtttgtgatacttactacttgagcactatgtg 780  
 781 ggtttcgtatgtcatgttaacgaatttgaacgaagaactttttaaaacactgcga 840  
 781 ggtttcgtatgtcatgttaacgaatttgaacgaagaactttttaaaacactgcga 840  
 841 gattacaatgttcaagcttattctgtacgcactgttgcgaatttcttataagaatt 900  
 841 gattacaatgttcaagcttattctgtacgcactgttgcgaatttcttataagaatt 900

841 gattacaatgttcaagcttattctgtacgcactgttgcgaatttcttataagaatt 900  
 901 gaattctcgataataatattttatacaaatattgttgaattgcatctgacgagacact 960  
 901 gaattctcgataataatattttatacaaatattgttgaattgcatctgacgagacact 960  
 961 ttactcaagaatattgttgagcgtgtgtcagacggtttaaattacgggtgtcgtcaa 1020  
 961 ttactcaagaatattgttgagcgtgtgtcagacggtttaaattacgggtgtcgtcaa 1020  
 1021 gactatggttttaacagaacaacactctgcacattatatacaccgcgaagaagcgatgataa 1080  
 1021 gactatggttttaacagaacaacactctgcacattatatacaccgcgaagaaga 1080  
 1081 ccaggtgcttctgcgaagaatgtgccaattttaagaacaaacttaccgtcttgatc 1140  
 1081 ccaggtgcttctgcgaagaatgtgccaattttaagaacaaacttaccgtcttgatc 1140  
 1141 aaaaaaacttggccgcgaacacagctgagaaagttgtgttaaagggtccatgctatg 1200  
 1141 aaaaaaacttggccgcgaacacagctgagaaagttgtgttaaagggtccatgctatg 1200  
 1201 aaaggtatgtatataatccagaagcaacaagaagaatcatagatgaagaagttggtg 1260  
 1201 aaaggtatgtatataatccagaagcaacaagaagaatcatagatgaagaagttggtg 1260  
 1261 cacacaggagatattgtgattacgattgaagaacaaacttcttaccgtgagatctg 1320  
 1261 cacacaggagatattgtgattacgattgaagaacaaacttcttaccgtgagatctg 1320  
 1321 aagctttaaatacaatacaagaagatatacaagtaacacactctgataatgatactgctt 1380  
 1321 aagctttaaatacaatacaagaagatatacaagtaacacactctgataatgatactgctt 1380  
 1381 ttgcacacatccactactacttctgtatgtgtgtgtgcggcggttccatgactgtgagc 1440  
 1381 ttgcacacatccactactacttctgtatgtgtgtgtgtgcggcggttccatgactgtgagc 1440  
 1441 gaagctccggagagctgtgtgttacttaagaagaagaatactatgactgaaagaagta 1500  
 1441 gaagctccggagagctgtgtgttacttaagaagaagaatactatgactgaaagaagta 1500  
 1501 atgattatgttgcaagtcgaagtttcaaatgcaaaacgtttacgtgtgtgtgtttt 1560  
 1501 atgattatgttgcaagtcgaagtttcaaatgcaaaacgtttacgtgtgtgtgtttt 1560  
 1561 gtgagcgaaggtacttaaaaggttccactgtgtaaatgtgaacgtgaagaataaata 1620  
 1561 gtgagcgaaggtacttaaaaggttccactgtgtaaatgtgaacgtgaagaataaata 1620  
 1621 ctgaagaacaacagttgtctaagatg 1644  
 1621 ctgaagaacaacagttgtctaagatg 1644

RESULT 15  
 ID AA003801 standard; cDNA; 1644 BP.  
 AC AA003801;  
 DT 22-AUG-1990 (first entry)  
 DT 26-FEB-1993 (revised entry)  
 DE Recombinant luciferase gene.  
 KW Luciferase; ATP; E. coli; photon; ds.  
 OS Synthetic.  
 PN JP02065780-A.  
 XX 06-MAR-1990.  
 PD

XX 01-SEP-1988: 88JP-0216229.  
XX  
XX 01-SEP-1988: 88JP-0216229.  
XX  
(KIKK) KIRKOMAN CORP.  
XX  
XX WPI: 1990-113360/15.  
XX P-PSDB: AAR05788.  
XX  
XX Prepn. of luciferase -  
XX using *Escherichia* sp. bacteria contg. recombinant DNA.  
XX  
XX Claim 2: Page 416 + Fig 3; 20pp; Japanese.  
XX  
XX Prepn. of luciferase comprises culturing *Escherichia* sp. contg.  
XX recombinant DNA, and harvesting luciferase from the culture medium.  
XX The recombinant DNA is a vector DNA into which has been inserted the  
XX luciferase gene which has the nucleotide sequence below. Luciferase  
XX can be produced quickly and efficiently with an increased photon  
XX output, useful in assaying ATP.  
XX  
XX Sequence 1644 BP; 529 A; 276 C; 338 G; 501 T; 0 other;

Query Match 82.5%; Score 1356; DB 11; Length 1644;  
Best Local Similarity 89.1%; Pred. No. 0;  
Matches 1464; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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DB 1 atggaacaatggaagaatgaataatgtagtgcgtgaaccatttaccatt 60  
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DB 61 gaagagagatctctgagacacattgccaagtatgatcgatctgcaaaactgga 120  
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DB 121 gcaattccttactaaccgtacacattcgcgtgcgtacattacgtacgcgcgaatacttga 180  
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DB 241 ggcgtatgcagtgaaactgtgaagaattcttattctctgattagccggtttata 300  
QY 301 ggtgtaggtgttgacacacattggaattacacattacgtgaacgtgttcaagttta 360  
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DB 361 ggcattcttaagccaactgttattagttcttaaaaaagattagataaagtataact 420  
QY 421 gtcaaaaaacggttaactgtatttaaacattgttattatggaacgaagtgtat 480  
DB 421 gtcaaaaaacggttaactgtatttaaacattgttattatggaacgaagtgtat 480  
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DB 481 agaggtatcaatcaatggaacatttataaaaaaacacccaagaagtccaagga 540  
QY 541 tcaagtttaaaactgtagaagttaaccggaagaagaagttgtcttataaactct 600  
DB 541 tcaagtttaaaactgtagaagttaaccggaagaagaagttgtcttataaactct 600  
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DB 661 ttcttcacgctagagatcccaatttatgaaacccaagtcttcacacgagcagctattta 720  
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DB 721 actgtagaacatccatcattggttggtagtcttactacttaggtactactgtt 780  
QY 781 gttttcgtatgtgcagttaaagaatgtgaagaagaagctttttaaaacatgca 840  
DB 781 gttttcgtatgtgcagttaaagaatgtgaagaagaagctttttaaaacatgca 840  
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QY 901 gaatttcgataaataatgattatcaaatlttagtgaatltgcatctgcgagacact 960  
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QY 1201 aaagttatgtagaataatccagaagcaagaagaatcatalagatgaagaagttgtg 1260  
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DB 1321 aagcttcaatcaatacaaaaggaatcacaagtaacacattcttattgtcgaatcgtt 1380  
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QY 1501 atggtatcgtttagtgaatcaggttcaaatgcaaaacggttgcgtgtgtgtgtt 1560  
DB 1501 atggtatcgtttagtgaatcaggttcaaatgcaaaacggttgcgtgtgtgtgtt 1560  
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DB 1561 gtgagcaagtagtaacaggtctcactgtgtaaaattgaacggtlaagcaaatagaata 1620  
QY 1621 ctgagaagaacaggttgaagatg 1644  
DB 1621 ctgagaagaacaggttgaagatg 1644

Search completed: September 6, 2002, 19:38:41  
Job time: 10769 sec





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•  
•

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 15:17:17 ; Search time 113.65 Seconds  
(without alignments)  
3553.203 Million cell updates/sec

Title: US-09-581-241-3  
Perfect score: 1644  
Sequence: 1 atggaacacatgagacga.....agaacccagtctgaagatg 1644

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2\_6/ptodata/2/1na/5B\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/1na/6A\_COMB.seq:\*  
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6: /cgn2\_6/ptodata/2/1na/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1639.2	99.7	1644	US-09-111-752-13	Sequence 13, Appl
2	1636	99.5	1644	US-07-903-047-7	Sequence 7, Appl
3	1636	99.5	1644	US-09-380-061B-15	Sequence 15, Appl
4	1631.4	99.2	1908	US-08-460-934-8	Sequence 8, Appl
5	1631.4	99.2	1908	US-08-782-118-8	Sequence 8, Appl
6	1632.8	98.7	1704	US-08-460-934-5	Sequence 5, Appl
7	1622.8	98.7	1704	US-08-782-118-5	Sequence 5, Appl
8	1356	82.5	1644	US-07-675-211-1	Sequence 1, Appl
9	1356	82.5	1644	US-07-903-047-1	Sequence 1, Appl
10	1356	82.5	1644	US-08-076-042-1	Sequence 1, Appl
11	1356	82.5	1644	US-08-757-046A-3	Sequence 3, Appl
12	1356	82.5	1644	US-09-447-208-3	Sequence 3, Appl
13	1356	82.5	1644	US-09-135-988-3	Sequence 3, Appl
14	1356	82.5	1644	US-09-277-116-3	Sequence 3, Appl
15	1356	82.5	1644	US-08-597-274A-3	Sequence 3, Appl
16	1356	82.5	1644	US-09-380-061B-13	Sequence 13, Appl
17	1263.2	76.8	1656	US-09-111-752-8	Sequence 8, Appl
18	1040.8	63.3	1656	US-09-111-752-9	Sequence 9, Appl
19	1040.8	63.3	1656	US-09-111-752-9	Sequence 9, Appl
20	1014.4	61.7	2009	US-09-380-061B-17	Sequence 17, Appl
21	818.8	49.8	1725	US-09-380-061B-19	Sequence 19, Appl
22	745.8	45.4	5427	US-09-282-996-2	Sequence 2, Appl
23	745.2	45.3	1811	US-08-867-352-22	Sequence 22, Appl
24	745.2	45.3	1811	US-08-867-352-22	Sequence 22, Appl
25	745.2	45.3	5791	US-08-862-431-31	Sequence 31, Appl
26	745.2	45.3	5793	US-08-862-431-29	Sequence 29, Appl
27	745.2	45.3	5793	US-08-862-431-30	Sequence 30, Appl

28	745.2	45.3	5818	US-08-536-559A-3	Sequence 3, Appl
29	745.2	45.3	5819	US-08-536-559A-2	Sequence 2, Appl
30	745.2	45.3	5819	US-08-862-431-27	Sequence 27, Appl
31	745.2	45.3	5819	US-08-862-431-28	Sequence 28, Appl
32	745.2	45.3	5938	US-08-536-559A-4	Sequence 4, Appl
33	745.2	45.3	6092	US-08-536-559A-1	Sequence 1, Appl
34	745.2	45.3	6092	US-08-862-431-26	Sequence 26, Appl
35	745.2	45.3	11616	US-08-196-259-2	Sequence 2, Appl
36	744	45.3	1722	US-09-380-061B-1	Sequence 1, Appl
37	743.6	45.2	1650	US-08-354-240A-1	Sequence 1, Appl
38	743.6	45.2	2445	US-08-122-520C-8	Sequence 8, Appl
39	743.6	45.2	5620	US-08-793-170-21	Sequence 21, Appl
40	743.6	45.2	5620	US-08-892-873-21	Sequence 21, Appl
41	743.6	45.2	5620	US-09-334-765A-21	Sequence 21, Appl
42	743.6	45.2	5620	US-09-356-575E-21	Sequence 21, Appl
43	743.6	45.2	5620	US-09-333-820-21	Sequence 21, Appl
44	743.6	45.2	6044	US-08-316-950-18	Sequence 18, Appl
45	743.6	45.2	6044	PCT-US95-12642-18	Sequence 18, Appl

#### ALIGNMENTS

RESULT 1  
US-09-111-752-13  
; Sequence 13, Application US/09111752  
; Patent No. 6074859  
; GENERAL INFORMATION:  
; APPLICANT: HIROKAWA, KOZO  
; APPLICANT: KAJIYAMA, NAOKI  
; APPLICANT: MURAKAMI, SEIJI  
; TITLE OF INVENTION: MUTANT-TYPE BIOLUMINESCENT PROTEIN, AND  
; TITLE OF INVENTION: PROCESS FOR PRODUCING MUTANT-TYPE LUMINESCENT PROTEIN  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,  
; ADDRESS: P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/111,752  
; FILING DATE: 08-JUL-1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 7126-0009-0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1644 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; ORIGINAL SOURCE:  
; ORGANISM: Luciola lateralis  
; US-09-111-752-13  
Query Match 99.7%; Score 1639.2; DB 3; Length 1644;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1641; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db	61	gaagaggatctgcttgagacacaattgycgaagtatatatgatgatgatagcgaacttgcga	120
QY	121	gcaattgcttctaactaagcaacttaaccggtgctcgatatagaagtcgaacgaacttagaa	180
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Db	181	aaatcatgctcttcaggagaagagcctttaaagaatatatgatttggttgtaataatgaagaatt	240
QY	241	gcgtatgcaatgaaactgtgaaagaattcttatctcgtatgataagcggatttatla	300
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Db	601	tggagttcaaccgggttggccaaaaggtgtgcacacttactcatgaanaatttggctcaga	660
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Db	841	gattacaacaatgttcaagcgttatctctgtacacgaacttggttgcaattcttaatagaagt	900
QY	901	gaattacacgataatgatttataccaatttggttgaattgctcttgaggaacact	960
Db	901	gaattacacgataatgatttataccaatttggttgaattgctcttgaggaacact	960
QY	961	ttatctaaagaatltgltgaagcgtgtgtctcagaagctlttlaatlaaccgggttctgca	1020
Db	961	ttatctaaagaatltgltgaagcgtgtgtctcagaagctlttlaatlaaccgggttctgca	1020
QY	1021	ggctatggtttaaagaagaacaacctctgcgaattatatatacacccggaagggagatataa	1080
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QY	1081	ccaagtgcttccttggcacaagtttgctgcacattatlaagcaaaagtlatcgcttgcatact	1140
Db	1081	ccagtgcttccttggcacaagtttgctgcacattatlaagcaaaagtlatcgcttgcatact	1140
QY	1141	aaaaaaccttggcccgacaacagctggagaaatttggtlaaaggttccatgctatg	1200
Db	1141	AAAAAACCTTTGGGCCCGAACAGACTGGGAAGTTTGTTAAAGGGTCTATGCTTATG	1200
QY	1201	aaagttatglatagataatccagaagcaacagaanaatcalagatgaaaggttggttg	1260
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QY	1261	cacacagagagatatggggtatcacgatagaaagaaaacatttctatcgtggatcgtttg	1320
Db	1261	CAcAcAGGAGATATTTGGATTCGATGAAAGAAAACATTTCCTTAACGCGGATCGTTTG	1320
QY	1321	aagcttctatcaaatcaaaaagatatcaagtaaccactgtaattagatcgtgtctt	1380
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QY	1381	ttagcaacatccacaatatlttttgaatgcggggtctgcttgcgtttccagatcccatagctgtg	1440
Db	1381	TtGCAACATCCAAATATTTTTGATGGCGGGGCTGTGGGCTTCCAGATCCTATAGCTGTG	1440
QY	1441	gagcttcggggagctgtgtgttacttaagaaagaaatctatgactgaaagaaagta	1500
Db	1441	GAGCTTCGGGAGCTGTTGTTGACTTAAGAAAAGAAAACCTATGACTGAAAAAGAAAGTA	1500
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QY	1561	gttgcagaaagtaacctaaaggtctccactgtgttaaatltgacgttlaagaaatlaagaata	1620
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Db	1621	CTGAAGAAACCAgTtGCTTAAGATG 1644	

RESULT 2  
 US-07-903-047-7  
 ; Sequence 7, Application US/07903047  
 ; Patent No. 5229285  
 ;  
 ; GENERAL INFORMATION:  
 ;  
 APPLICANT: Kajiyama, Naoki  
 APPLICANT: Nakano, Eiichi  
 TITLE OF INVENTION: Thermostable Luciferase Of Firefly,  
 TITLE OF INVENTION: Thermostable Luciferase Gene Of Firefly, No. 5229285el Recd  
 TITLE OF INVENTION: DNA, And Process For The Preparation Of Thermostable  
 TITLE OF INVENTION: Luciferase Of Firefly  
 NUMBER OF SEQUENCES: 11  
 ;  
 ; CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennile & Edmonds  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 ;  
 ; COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/903,047  
 FILING DATE: 19920623  
 ;  
 CLASSIFICATION: 435  
 ;  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mistrock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 7005-048  
 ;

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8664/9741

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1644 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: cDNA to mRNA

US-07-903-047-7

Query Match 99.5%; Score 1636; DB 1; Length 1644;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 61 GAAGAGAGATCTGTGAGACACATTTGCGCAAGTATATGATGATGCAATGCAAAACTTGA 120
Qy 121 gcaatgtcttactaaagccttaacgggtgtgattataatgatacgcgaacttga 180
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Qy 181 aaatcatctgtctagaagagagcttaagaattatgtgtgtgtgtatgtagaagatt 240
Db 181 AAATCATCTGTCTAGAAGAGAGCTTAAAGAATTATGTTGTGTGTGATGAGAAAGATT 240
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Db 241 GCGTATGACATGTAAGAACTGTGAAGAAATTCTTATCCCTGATTAGCGCGTTTATTATA 300
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Db 361 GGCATCTCTAAGCCACACATTTGTTAGTTCTAAAAAAGATTAGATAAAGTTATAACT 420
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Db 421 GTACAAAAACGGTAACTGCTATTAAAAACATTGTTATTGACAGCAAGTGGATTAT 480
Qy 481 agaggtatcaatcaatgacacacttataaaaaaacatcccaaggtttcaaga 540
Db 481 AGAGGTATCAATCAATGACACACTTATATAAAAAAACACTCCACAAAGTTTCAAGA 540
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Db 661 TTTTCTACGCTGAGATCCAAATTTATGAAACCAAGTTTACACGAGCGCTATTATTA 720
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Qy 781 gggttcgtatgtcaatgtaagaatttgaagagaagactttttaaaacactgca 840
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Qy 841 gattacaatgttcaagcgttatcttctgtaaccgactttgtgcaattcttaagaagt 900
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Qy 1081 ccaggtgctctgtgcgaagttgtgcattatattaaagcacaagtatacgtacttga 1140
Db 1081 CCAAGTGTCTTGTGCAAGTTGTGCATTATTAAAGCAAAAGTTATGCAATCTGTACT 1140
Qy 1141 aaaaaaaccttgggcccgaagacgttgaagaagttgtgtaaggttccatgctatg 1200
Db 1141 AAAAAAATCTTGGGCCCGCAACAGACGTGGAAGTTGTGTAAGGCTCTATGCTATG 1200
Qy 1201 aaagttatgtatgaataatccagaagcaacagaagaataatagatgaagaagttgtg 1260
Db 1201 AAAGTTATGTAGTAAATCCAGAACACAGCAAGAAATCTAGATNAGAAAGTTGGTG 1260
Qy 1261 cacacagagataatggatlaacatgaagaacaaacattcttactcgtggaatcgtt 1320
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Qy 1621 ctgaagaacacagttgtctaagatg 1644
Db 1621 CTGAAGAACACAGTTGCTAAGATG 1644

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# RESULT 3

US-09-380-061B-15  
Sequence 15, Application US/09380061B  
Patent No. 6265177

## GENERAL INFORMATION:

APPLICANT: SOUTRELL, DAVID JAMES

WHITE, PETER JOHN

LOWE, CHRISTOPHER ROBIN

MURRAY, JAMES AUGUSTUS HENRY

TITLE OF INVENTION: ENZYME ASSAY FOR MUTANT FIREFLY LUCIFERASE

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSER: NIXON & VANDERBYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON



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OY      1561 gttgacgaagtagctaaaggcttcaccgcgtgaataattggcagttaaacacttggagaana 1620
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RESULT          4
US-08-460-934-8
Sequence 8, Application US/08460934
Patent No. 5814465
GENERAL INFORMATION:
APPLICANT: TATSUMI, HIROKI
APPLICANT: FUKUDA, SATOSHI
APPLICANT: KIKUCHI, MAMORU
APPLICANT: KOYAMA, YASUJI
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINATED AND A BIOLUMINESCENT
TITLE OF INVENTION: ANALYSIS METHOD
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,934
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 98857/1995
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLOD, NORMAN E.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-001-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1908 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1908
OTHER INFORMATION: /note= "The nucleotide sequence of
OTHER INFORMATION: the biotinylated firefly luciferase gene contained in
OTHER INFORMATION: recombinant plasmid pHLf248 DNA"
NAME/KEY: CDS
LOCATION: 1..1908

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[illegible]

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QY 1441 gagcttcggagagctgtgtgttacttaagaagaagaactctatgaactgaagaagta 1500
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RESULT 5
US-08-782-118-8
; Sequence 8, Application US/08782118
; Patent No. 583746
; GENERAL INFORMATION:
; APPLICANT: TATSUMI, HIROKI
; APPLICANT: FUKUDA, SATOSHI
; APPLICANT: KIKUCHI, MAMORU
; APPLICANT: KOYAMA, YASUJI
; TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE
; TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A
; TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P. C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,118
; FILING DATE: 13-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/460,934
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: JP 193798/1994
; FILING DATE: 27-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 54625/1995
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 98857/1995
; FILING DATE: 24-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 7126-001-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1908 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1..1908
; OTHER INFORMATION: /note="the nucleotide sequence of
; OTHER INFORMATION: the biotinylated firefly luciferase gene contained in
; OTHER INFORMATION: recombinant plasmid pHLf248 DNA"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1908
; US-08-782-118-8

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Query Match 99.2%; Score 1631.4; DB 2; Length 1908;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1635; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 atgaaaaacatggaagacgataaataatgtgatggtcgcgaacattaccctatt 60
    |||||||
DB 1 atgaaaaacatggaagacgataaataatgtgatggtcgcgaacattaccctatt 60
QY 61 gaagaaggatctgtagacacacatgacgaaglatatgtagatcgatgcaaaactgga 120
    |||||||
DB 61 gaagaaggatctgtagacacacatgacgaaglatatgtagatcgatgcaaaactgga 120
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DB 121 gcaattgctttactaaagcaactaccggtgltcgaltatacgtacgcgaataactga 180
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QY 241 ggcatacagtgaaacacgltgaagaatcttatacccggtatgaacgggttattata 300
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DB 241 ggcatacagtgaaacacgltgaagaatcttatacccggtatgaacgggttattata 300
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DB 301 ggtgtcgtgtggtcctcaactaagatgagattacactcagtgaaattggttcaagtt 360
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DB 361 ggcattctaaagcaaaactgtattatgattctaaagaaggtttagataaacttaact 420

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Db	421	GTACAAAAACGGTAACCTGCTATTAAACCAATTGTTATATTGGACAGCAAAAGTGATATAT	480
QY	481	agaagttatcaatcccatggacaactcttataaaaaaacactcccaaggtcttcaagga	540
Db	481	AGAGGTTATCAATCCATMGAGCAACCTTTATTAAAAAAAACACTCCACAGGTTCCAAAGGA	540
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QY	601	tccggttccaacccggtttgccaaaaggctgacgaacttactcaatgaattttgttaactaga	660
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QY	661	tttctcaactagatcccaatttatggaaaacaaagtttcaaccgaacgcgcatattta	720
Db	661	TTTTCTCAGCGCTAGAGATCCCAATTTATGSAAMCAAGTTTACCGACGACGGCATTTTTA	720
QY	721	actgttagtaccatltccatcaatggttltgtatgttactacttaaggctatctaatgtt	780
Db	721	ACTGTATACCAATTCATCATGATGGTTTGGTATGTTTACTACTTGGCTATCTAACTGTGT	780
QY	781	ggtttcgtatgttcagttaaagaaatttgcggaagagactttttaaaaaacctgcga	840
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QY	841	gattacaactgttcaacgcgtatcttcttgcacgaacttgttgcgaactcttaatagaat	900
Db	841	GATTACAATAGTTCACGCGTATTCTTGTACCGACTTGTTCGCAATCTTAATAGAAAT	900
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QY	1021	ggtcatgttttaacagaanaaacactctctgcgaattatataccaaccggaagcgatgataa	1080
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Db	1261	CACACAGAGAGATATTGGGCTTATACGATGAAGAAAAACAATTTCTTATGCTGATGCTTGG	1320
QY	1321	aagctttaaatacaatacaagaagatatacaagtaacacactgtcgtaattagaatctgtctt	1380
Db	1321	AAGCTTTTAATCAAAATCAAAAGATATCAAAAGTACCCACTGCTGAATTAAGAAATCTGTTCT	1380
QY	1381	tttgaacatccaatatctttttagtcgcgcggttgcgtgcggttcgaatctcctatagctgtg	1440
Db	1381	TTTGACATCCAAATTAATTTTGTATGTCGGGGGCTTGTGCTTCAGATCTCATATACCTGTGT	1440
QY	1441	gagcttccggagagctgttctgttacttaagaagaagaaatcatgacatgaaaaaaaagta	1500
Db	1441	GAGCTCCGGGAGCTGTGTGTGTACTTTGAAGAAAGGAAATCTATGACTGAAAGAAACAAATA	1500
QY	1501	atgagattacgttctgtagtaagtttccaatatgcaaaaacgtttgcgtgtgtgtccgttctt	1560

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Qy	901	gaatttcgcataaattgtttattcaaatllagtttgaattgcacctcggcgagcact	960
Db	901	GAATTACTCATAAATATCGATTTGTCTCAAAATTATAGTTGCAATTGCGCGAGCACT	960
Qy	961	ttatctaaagaattgvtgaagctgtgtctagaagllttaattcaaccgggtgtcgloca	10200
Db	961	TTATCTCAAAAGAGTTGGTGAAGCTGTGTTCTACAGCGCTTAAATCTCCCGTCTTGCTAA	10200
Qy	1021	ggtcatggtttaaacaagaacaacctctgcacattatctacaacggaaagcagatataa	10800
Db	1021	GGTATGGTTTAAACAGAAACACATCGTCGATATATTATACACAGAAAGAGACGATAAA	10800
Qy	1081	ccaagtcgtcttcgccaagttgtgcattatlttaaagcaaaagttatcgattctgaact	11400
Db	1081	CCAGAGAGCTCTCGAANAAGTCGCGCGTCTTTAAAGCAAAAGTATTCATCTTATATACC	11400
Qy	1141	aaaaaaactttgggcccgaacagacgltgagaaagtttgttgaagggltcctactgtta	12000
Db	1141	AAAAAACTTTAGGTCTCTAACACACGCGGAGGAAGTTGTGTTAAAGACCTATGCTATWG	12000
Qy	1201	aaaggttatgtagaatccagaagaacaagaagaaatcatatgatagaagaagttggttg	12600
Db	1201	AAAGGTATGTGAATATATCCAGAGACACAAAAAGAACTTATGACGAGAAAGATGTGGCTG	12600
Qy	1261	cacacagagatatltggtattlaagatlgaaagaaaaaatlcttlatcgttgatcgtttg	13200
Db	1261	CACACCGGAGATATTTGGATATATATGATGAAGAAAAACATTTCTTATATGTGCATGCTTG	13200
Qy	1321	aagctttaaataaatacaagaagatbtaagtaacgcgcgtgaattgaatcgttctt	13800
Db	1321	AAGCTTTAATCAATATCAAGAGATACCAAGTACCAAGCTGCGGAATATGAAATCGCTTCTT	13800

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1      COMPUTER:  IBM PC compatible
2      OPERATING SYSTEM:  PC-DOS/MS-DOS
3      SOFTWARE:  PatentIn Release #1.0, Version #1.25
4      CURRENT APPLICATION NUMBER:  US/08/076.042
5      APPLICATION NUMBER:  US/08/076.042
6      FILING DATE:  15-JUN-1993
7      CLASSIFICATION:  435
8      PRIOR APPLICATION DATA:
9      APPLICATION NUMBER:  US 07/675,211
10     FILING DATE:  26-MAR-1991
11     NAME:  435
12     ATTORNEY/AGENT INFORMATION:
13     NAME:  MISROCK, S. LESLIE
14     REGISTRATION NUMBER:  18,872
15     REFERENCE/DOCKET NUMBER:  7005-026-999
16     TELECOMMUNICATION INFORMATION:
17     TELEPHONE:  212-790-9090
18     TELEFAX:  212-869-9741
19     TELEX:  66141 PENNIE
20     INFORMATION FOR SEQ ID NO. 1:
21     SEQUENCE CHARACTERISTICS:
22     LENGTH: 1644 base pairs
23     TYPE: nucleic acid
24     STRANDEDNESS: single
25     TOPOLOGY: linear
26     MOLECULE TYPE: cDNA
27     ORIGINAL SOURCE:
28     ORGANISM:  Luciola cruciata
29     FEATURE:
30     NAME/KEY:  CDS
31     LOCATION:  1..1644
32     US-08-076-042-1

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1 RESULT 10
2 US-08-076-042-1
3 : Sequence 1, Application US//08076042
4 : Patent No. 5330906
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: KAJIYAMA, NAOKI
9 :
10 : APPLICANT: NAKANO, EIICHI
11 :
12 : TITLE OF INVENTION: MUTANT LUCIFERASE OF A FIREFLY, MUTANT
13 :
14 : TITLE OF INVENTION: LUCIFERASE GENES, NOVEL RECOMBINANT DNAs CONTAINING THE
15 :
16 : TITLE OF INVENTION: GENES AND A METHOD OF PRODUCING MUTANT LUCIFERASE
17 :
18 : NUMBER OF SEQUENCES: 4
19 :
20 : CORRESPONDENCE ADDRESS:
21 :
22 : ADDRESSEE: PENNIE & EDMONDS
23 :
24 : STREET: 1155 AVENUE OF THE AMERICAS
25 :
26 : CITY: NEW YORK
27 :
28 : STATE: N.Y.
29 :
30 : COUNTRY: U.S.A
31 :
32 : ZIP: 10036
33 :
34 : COMPUTER READABLE FORM:
35 :
36 : MEDIUM TYPE: Floppy disk

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Query Match	Best Local Similarity	82.5% Matches 1464	Score 1356	DB 1	Length 1644
QY	1	atggaacacatgagaaacatgaaataatgtgtatggtcctcgaacacattaccctatt	60		
Db	1	ATGGAAMACATGGAAMACGATGMAATATTTGATTTGGACCTTAAMCCGTTTAACTTACC	60		
QY	61	gaagaggatctgctctgagacacaattgcgcgaagtatatgatacgataigcaaaacttga	120		
Db	61	GAAGGGGATCTGCTCGGAACACAAATTAAGCAAAATACATGAGACCGATATGCAAAACTTGGC	120		
QY	121	gcaattgcttttactcaacgacactaccggtgtgcgatttaagtaagccgaactactaga	180		
Db	121	GCAATTTGCTTTTACAAATGACACTTACTGTGTGTTATTTCTTAAGCCGGAATACTTTGGAG	180		
QY	181	aaatcatcgtcttctatgagagagcctttaaagaattatggtlttglttgatgaaagaatt	240		
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QY	241	gcgtatgacagtgaanaacttgcgaagaattcttattcctgtatagccggtttattata	300		
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QY	301	ggtgtcgtgtggtgcctcaactaatbaagtttaacctacgtacagtgaaattggttcaagttta	360		
Db	301	GGTGTAGGTGTGTGACCCCACTTAATAGATTTTACACTTTAACGTAACGGTTCACAGTTTA	360		
QY	361	ggcaatcctaaagccaacatgatacttattagttcctaaagaagatagataaagtataact	420		
Db	361	GGTACTCTTAAACCAACAACTTGTATTAGTTGTATAAAAAGCGTTAGATTAATTTTAAACA	420		
QY	421	gtacaaaaacgtaactgtctattaaacacatgltatattatgagacgaagaatgtgattat	480		
Db	421	GTACAGAAACAGTACTACTATTAAACCACTTGTATTACTAGTATGACCAAAAGTTGATTAT	480		
QY	481	agaggttatcaatccatgagacaacttattaaaaaaaacctcccaagaagtlttcaaaaga	540		
Db	481	CGAGATATTCATATGTCGTGGACACCTTTTATAAAAACCAACCTCCACCGAGTTTCAAGCA	540		



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QY 241 gcgtatgcagtgaaaactgtgagaactcttattctcigtatlaagccggttattata 300  
Db 241 GCGTTATGACGTAACAACTGTGAAGAAATTTTATTCCTGTAATACCGGACGTGTATA 300  
QY 301 ggtgtcgtgtgtgtcccaactaagatgatttaactctcagtaattgtgtccagttta 360  
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QY 361 ggcattccaaagcaaatgttattagtttccaaaagagattagataaagtataact 420  
Db 361 GGTATGTCATAACCAACAAATTTGATTAGTTCAAAAAAGCGTTAGATAAGTTATATACA 420  
QY 421 gtacaaaacacgttaactgtctatlaaacacattgttatalatgagcagcaagtgtatlat 480  
Db 421 GTACAGAAAACAGTACTACTATTAAACCATTTGTTATACATAGATGCAAAAGTTGATTAT 480  
QY 481 agaggttatcaatccatgagcaacttatataaaaaaacctccacaagttccaagaa 540  
Db 481 CGAGGATTCATCAATGCTGTGACACCTTTATATAAAGAAACACCTCCACGAGGTTTCAAGCA 540  
QY 541 tcaagttttaaactgtagaagttaaacgaaagatgtgccttataatgaactc 600  
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QY 661 ttctccacgctagagatcccaatttatgagaacaaagttccaccagcagcgctatttta 720  
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QY 1021 ggcattgattttaaacaacaacctctgcaattatataccaccggaagcagatgataa 1080  
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QY 1081 ccaagtgcttctgtgcaaggtgtgtccattattaaagcaaaagtatcgattgact 1140  
Db 1081 CCAAGGAGCTTCTGAAAAGTCGCGCTGTTTAAAGCAAAAGTTATGATCTTGATATAC 1140  
QY 1141 aaaaaaacttggcccgagacagcgtgagaagttgtgtaagaggtcctatgctatg 1200  
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QY 1201 aaaggtatgataataccagaagcaacaagaagaaatcatalagatgaagaaggtgtgt 1260  
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QY 1261 cacacagagatatgtgattatcagatgaagaanaacatttcttactcgtgtgtgt 1320  
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QY 1621 ctgaagaacacagttgtctaagatg 1644  
Db 1621 CTTAAGAAACAGTGTCTAAGATG 1644

RESULT 12  
US-09-447-208-3  
; Sequence 3, Application US/09447208  
; Patent No. 6113886  
; GENERAL INFORMATION:  
; APPLICANT: Bryan, Bruce  
; TITLE OF INVENTION: BIOUMINESCENT ARTICLES OF MANUFACTURE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; STREET: 4250 Executive Square, 7th Floor  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/447, 208  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 0909/135, 988  
; FILING DATE: 08-17-98  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/757, 046  
; FILING DATE: 11-25-96  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/597, 274  
; FILING DATE: 02-06-96  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L.  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 24727-105C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-450-8400  
; TELEFAX: 619-450-8499  
; TELEX:  
; INFORMATION FOR SEQ. ID NO.: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1644 base pairs



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: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: Coding Sequence
: LOCATION: 1..1644
: OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)
: PUBLICATION INFORMATION:
: US-09-447-208-3

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Query Match 82.5%; Score 1356; DB 3; Length 1644;

Best Local Similarity 89.1%; Pred. No. 0;

Matches 1464; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

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QY 1 atggaacacatggaacacatgataatattgtatgtgtccctgaaccattaccatt 60
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QY 241 gcgatgacatggaacacatggaacacatcttacttctgtatagacggttactata 300
Db 241 GCGTATGCACTGAAACTGTGAAGATTTTATTCCTGTAATAGCGCGACTTTTATA 300
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QY 361 ggcattcctaaagcaaatgtatgtatgtcttaaaaaaggaatagataagttact 420
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Db 421 GTACAAAACAGTAACACTATTAAAAACATGTTTATCTAGATGACCAAGTTGATTTAT 480
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Db 481 CGAGATATCAATGTCTGACACCTTTATATAAAGAAACACTCCACAGTTTCAAGCA 540
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Db 1081 CCAGGAGCTTCTGGAAGATCTGCGCTGTTTAAAGCAAAAGTTATTTGATTTGATACC 1140
QY 1141 aaaaaacttggcccgacagacgctggagaagtttgtaagaggtcctatgctatg 1200
Db 1141 AAAAAATCTTTAGCTCTTAACAGACGCTGAGAAAGTTTGTGTTAAAGAGACCTATGCTTATG 1200
QY 1201 aaagttatgtatgataatccagaagcaacaagaagaatcatalagatgaagaagttggt 1260
Db 1201 AAAGTTATGTTAATATATATCAGAACACAAAGAACTTATTGACGAAAGAGTTGGCTG 1260
QY 1261 cacacagagatatttggtatgataagaaagaaacacattcttatacgtgactgttg 1320
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QY 1321 aagcttctaatacaatacaagaagataatcaagtacacacgctgcaatttgaatctgtct 1380
Db 1321 AAGCTTTTATCAATATACAAAGGATACCAAGTACACACCTGCGGAATATTAATCCGTTCT 1380
QY 1381 ttgcaacatccaaatatttltgacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
Db 1381 TTGCAACATCAATCAATCTTTGATGCTGCTGTTGCGCGGCTTCTGATCTGATGCTGCG 1440
QY 1441 gacgtccggagatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1500
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QY 1561 gtgacggaagttactaaaggtctcactgtglaaaattgacggtlaaagcaatagagaata 1620
Db 1561 GTGATGAAAGTACTTAAGGTCTTACTGGAATAATTGACGCGCAGACATTTAGAGAAATC 1620
QY 1621 ctgaagaacacgctgtcgaagtgtg 1644
Db 1621 CTTAAGAAACCACTGTCTAAGATG 1644

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RESULT 13
US-09-135-988-3
: Sequence 3, Application US/09135988
: Patent No. 6152358
: GENERAL INFORMATION:
: APPLICANT: Bryan, Bruce
: TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Heller Hirman White & McAnuliffe
: STREET: 4250 Executive Square, 7th Floor
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/135,988  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/757,046  
FILING DATE: 11-25-96  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/597,274  
FILING DATE: 02-06-96  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24727-105C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-450-8400  
TELEFAX: 619-450-8499  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1644 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...1644  
OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)  
PUBLICATION INFORMATION:  
US-09-135-988-3

Query Match 82.5%; Score 1356; DB 3; Length 1644;  
Best Local Similarity 89.1%; Pred. No. 0;  
Matches 1464; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 1 atggaaacacatgagagacgataaataatgtgtatgtgtccgaaccatttaacctatt 60  
DB 1 AAGGAAACATGATGGAACATGAAATGATGAGTGAACCTAAACCGTTTACCCCTATC 60  
QY 61 gaagagagatcgcctgagacacatgacagatgatatgatcgatgatacaaaacttga 120  
DB 61 GAAGAGGATCTGCTGGAACACATTAACCAATACATGAGCGATATGCAAAACCTTGGC 120  
QY 121 gcaattgcttctactaacgacacttaccggtgtcgtatctacgtacgcgaacttagaa 180  
DB 121 GCAATGCTTTTACAATATGACAGTACTGCTGATTGATTCTTACGCCGATCTTGAG 180  
QY 181 aataatcgtcgtctagagagagccttaagaattatggttgggtgtgtatggaagaatt 240  
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DB 541 TCCAGTTTCAAACTGTGGAAGTTGACCGTAAGAACAAAGTCTCTTATTAATGAACCTC 600  
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DB 601 TCGGGTTTTCACGGTTTGCAGAAAGCGTACCACTTACGAAATATACGATCCTAGCA 660  
QY 661 ttcttcaacgttagagatccaatttaltgaaacaaagttccacagcgcgctattta 720  
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QY 721 actgtatgatacctcatcatcattgttggatgttactactttaggtatcactatctgt 780  
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QY 781 ggtttcgtatgttcaatgttgaagaatttgaagaagagactttttaaanaacgtgcaa 840  
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QY 901 gaattacgtataaataatgattatcaaatlttagttgaattgtcatctgacgagacact 960  
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RESULT 14  
US-09-277-

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? Sequence 3, Application US/09237716A
? Patent No. 6232107
? GENERAL INFORMATION:
? APPLICANT: Bryan, Bruce
? APPLICANT: Szent-Gyorgyi, Christopher
? APPLICANT: PROLUME, LTD.
? TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
? CURRENT APPLICATION NUMBER: US/09/277,716A
? CURRENT FILING DATE: 1999-03-26
? EARLIER APPLICATION NUMBER: 60/102,939
? EARLIER FILING DATE: 1998-10-01
? EARLIER APPLICATION NUMBER: 60/089,367
? EARLIER FILING DATE: 1998-06-15
? EARLIER APPLICATION NUMBER: 60/079,624
? EARLIER FILING DATE: 1998-03-27
? NUMBER OF SEQ ID NOS: 32
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 3
? LENGTH: 1644
? TYPE: DNA
? ORGANISM: Luciola cruciata
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(1644)
? FEATURE:
? OTHER INFORMATION: Luciola cruciata (firefly) luciferase
? PUBLICATION INFORMATION:
? PATENT DOCUMENT NUMBER: 4,968,613
? PATENT FILING DATE: 1988-07-26
? PUBLICATION DATE: 1990-11-06
? US-09-277-716-3

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				Gaps 0;

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QY 241 gcgtaatgcagtgaaacattggaagattcttattcttcgtatttaagccggtattatara 300  
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QY 361 ggcattccttaagccaacaattgtattagtcttaaaaaagattatagataaagtataact 420  
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Db	361	ggatctcttaaaccaacaacaaattgtaattgaattccttaaaaaagccttagataaagtattaca	420
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QY	961	ttatctaaagaagaattgttgagacgctgtgtgcagacgcttttaatttcacgggtttctgtaa	1020
Db	961	ttatccaaaagaagttgttgagacgctgtgtgcagacgcttttaactctcccggtgtctgta	1020
QY	1021	ggctatggtttaacagaacaaacctctgcacattatatacacccggaagcgatgataaa	1080
Db	1021	ggttatggtttaacagaacaaacctctgcacattatattataccagaagcgagagataaa	1080
QY	1081	ccaagttgctctcgcgaagttgtgccaattatttaaagcaaaagttatcgactctgtact	1140
Db	1081	ccaaggaactctcgcgaagaagctgcgcgcgtgtttaaagcaaaagttatgactctgtatacc	1140
QY	1141	aaaaaaactttggcccgcaacacgaacgltgtagaagtttgtgataaggtctactgcttga	1200
Db	1141	aaaaaacttttaggtctctaaccagacgltgtagaagtttgtgataaggaactatgcttga	1200
QY	1201	aaaagttatgtatgataatccagaagaacacaaagaatacatgataatgaaagaagttgtctg	1260
Db	1201	aaaagttatgtataaataatccagaagaacacaaagaactatattgcagaaagaagttgtcgtg	1260
QY	1261	caccacgagatattgttgatactttagcgtggaanaaaacatttcttatacgtgatcgtctg	1320
Db	1261	caccacggagatattgttgatactttagcgtggaanaaaacatttcttataatgcatcgtctg	1320
QY	1321	aagctcttaatacaaatatacaaaagatatcaagtaaccaactgcgcgaataatgaatccgttct	1380
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QY	1381	tttgaacatccaataattttttagtcgcgcgcgttgcgttgcgttccagatcttataagctgt	1440
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RESULT 15  
US-08-597-274A-3  
; Sequence 3, Application US/08597274A  
; Patent No. 6247995  
; GENERAL INFORMATION:  
; APPLICANT: Bryan, Bruce  
; TITLE OF INVENTION: BIOLUMINESCENT NOVELTY ITEMS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Brown, Martin, Haller & McClain  
; STREET: 1660 Union Street  
; CITY: San Diego  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92101-2926  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/597, 274A  
; FILING DATE: 02/06/96  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seidman, Stephanie L  
; REGISTRATION NUMBER: 33,779  
; REFERENCE/DOCKET NUMBER: 6680-105  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-238-0999  
; TELEFAX: 619-238-0062  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1644 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 1...1644  
; OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)  
; PUBLICATION INFORMATION:  
; DOCUMENT NUMBER: 4,968,613  
; US-08-597-274A-3

Query Match 82.5%; Score 1356; DB 4; Length 1644;  
Best Local Similarity 89.1%; Pred. No. 0;  
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Search completed: September 6, 2002, 19:29:53  
Job time: 15156 sec



GenCore version 4.5  
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# OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 15:07:47 : Search time 3537.97 Seconds  
(without alignments)  
6271.674 Million cell updates/sec

Title: US-09-581-241-3  
Perfect score: 1644  
Sequence: 1 atggaacacatgagagacga.....aggaacacatgctgaatg 1644

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estnu:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	199.4	12.1	768	10 BM412281	BM412281 EST586608
3	198.2	12.1	667	9 A1486799	A1486799 EST245121
4	190.4	11.6	651	10 C90519	C90519 C90519 Dict
5	189.8	11.5	582	9 AM621420	AM621420 EST312218
6	185.8	11.3	625	9 A1485586	A1485586 EST243907
7	183.2	11.1	569	9 AM218471	AM218471 EST303654
8	181.6	11.0	522	9 A1488821	A1488821 EST247160
9	173.8	10.6	543	10 BE555239	BE555239 sp87a10.y
10	173.6	10.6	612	10 BG130292	BG130292 EST475938
11	171.8	10.5	606	10 B1923203	B1923203 EST543107
12	165.6	10.1	741	9 AU214129	AU214129 AU214129
13	162.4	9.9	535	9 A1389862	A1389862 MTRC57409
14	162.2	9.9	498	10 B1425803	B1425803 sah72f03.
15	162.2	9.9	570	10 BG791252	BG791252 ESTFNL115
16	161.4	9.8	548	10 BM188336	BM188336 sa199f03.
17	159.4	9.7	604	9 AU219684	AU219684 AU219684

18	159.4	9.7	604	9 AV558307	AV558307
19	158.8	9.7	520	10 B1269977	B1269977 NF003D02F
20	158.8	9.7	638	9 AU214473	AU214473 AU214473
C 21	158.2	9.6	712	9 AM349844	AM349844 GM210006A
C 22	158	9.6	611	10 B129072	B129072 B129072
C 23	157.8	9.6	644	10 B1309413	B1309413 EST330823
C 24	157.8	9.6	722	10 B1339943	B1339943 B1339943
C 25	157.6	9.6	590	9 AM329421	AM329421 N2006566
C 26	157.4	9.6	558	9 AV680327	AV680327 AV680327
C 27	157.4	9.6	567	10 BG580544	BG580544 EST482271
C 28	157.4	9.6	656	9 AM691106	AM691106 NF041C08S
C 29	154.8	9.4	410	10 BM109695	BM109695 EST557231
C 30	154.8	9.4	977	12 CNG01MDU	AL150803 Anopheles
C 31	152.2	9.3	808	9 AM348381	AM348381 GM210002A
C 32	150.2	9.1	540	9 A1771202	A1771202 EST252398
C 33	149.6	9.1	506	9 AM132800	AM132800 se10411.y
C 34	149.6	9.1	529	10 BM143081	BM143081 sb56d11.y
C 35	148.8	9.1	377	9 A1938631	A1938631 sb56d11.y
C 36	148.8	9.1	655	9 AM560940	AM560940 EST315988
C 37	148.6	9.0	453	10 BF005122	BF005122 EST433620
C 38	148.6	9.0	405	9 AU284477	AU284477 AA3B-AA3Y
C 39	147	8.9	508	9 AM423914	AM423914 SH57907.Y
C 40	146.2	8.9	683	10 BF492687	BF492687 AT01136.3
C 41	145.8	8.9	565	10 BE330067	BE330067 so73a05.Y
C 42	145.8	8.9	665	10 BF200141	BF200141 WHE2252.E
C 43	145	8.8	595	9 AM329094	AM329094 N2003006
C 44	144.6	8.8	623	10 BF634495	BF634495 NF062809D
C 45	144.4	8.8	501	10 BG882703	BG882703 sae51e04.

## ALIGNMENTS

RESULT 1  
C83857  
LOCUS C83857  
DEFINITION C83857 Dictyostellium discoideum ss (H. Urushihara) Dictyostellium  
discoideum CDNA clone SSA391, mRNA sequence.  
C83857  
ACCESSION C83857  
VERSION C83857.1 GI:2706789  
KEYWORDS EST.  
SOURCE Dictyostellium discoideum.  
ORGANISM Dictyostellium discoideum  
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.

REFERENCE 1 (bases 1 to 664)  
Mori, T., Urushihara, H., Saito, T., Uga, Y., Mizuno, H., Yoshida, M.,  
Yoshino, R., Mitra, B. N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H.,  
Williams, J., Maeda, M., Takeuchi, I., Ochiai, H., and Tanaka, Y.  
The Dictyostellium developmental CDNA project: generation and  
analysis of expressed sequence tags from the first-finger stage of  
development

## TITLE

JOURNAL DNA Res. 5 (6), 335-340 (1998)  
MEDLINE 99156227  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan  
Email: d402huesakura.cc.tsukuba.ac.jp  
PROJECT = "Dictyostellium discoideum CDNA project in Japan"  
POLY-A-No.

FEATURES  
source location/Qualifiers  
1..664  
/organism="Dictyostellium discoideum"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="SSA391"  
/clone\_lib="Dictyostellium discoideum ss (H. Urushihara)"  
/dev\_stage="slug"

BASE COUNT 234 a 105 c 124 g 201 t  
ORIGIN

Query Match 12.7%; Score 208.6; DB 10; Length 664;





Db 752 GAAGTGAAGGATTCAT 768

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RESULT 3

LOCUS A1486799 667 bp mRNA linear EST 18-MAY-2001

DEFINITION EST245121 tomato ovary, TAMU Lycopersicon esculentum cDNA clone

ACCESSION A1486799

VERSION A1486799.1 GI:4382170

KEYWORDS EST.

SOURCE tomato.

ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

REFERENCE 1 (bases 1 to 667)

AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,D., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nieman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J.

TITLE Generation of ESTs from tomato carpel tissue

JOURNAL Unpublished (1999)

COMMENT Contact: CUGI

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES

source

1. 667

/organism="Lycopersicon esculentum"

/cultivar="TA496"

/db\_xref="taxon:4081"

/clone="CLEB11D3"

/clone\_id="tomato ovary, TAMU"

/tissue="carpel"

/dev\_stage="5 days pre-anthesis to 5 days post-anthesis"

/lab\_host="XLI-Blue MRF"

/note="Vector: pBlueScript SK(-); Site\_1: EcoRI; Site\_2: XhoI; CLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."

BASE COUNT 201 a 120 c 155 g 191 t

ORIGIN

Query Match 12.1%; Score 198.2; DB 9; Length 667;

Best Local Similarity 57.6%; Pred. No. 3.3e-35;

Matches 384; Conservative 0; Mismatches 268; Indels 15; Gaps 1;

Db 838 caaagatcaaatcttcaagcgttattctgtaccgacttggttgcaattcctaaga 897

||||| | | | |

Db 1 CAAATATTAGAGGTGACCATGAGGCCATTGTGCCACCTATTGTTGGCTAATGCTAAG 60

Qy 898 agtgaattaccgataataatgatattatcaaatatagttgaattgacatctggcgagca 957

||||| | | | |

Db 61 AGTCTATAGTTGATTAATTAATGATTATTCATCGGTGAACACCGTATGCTGGGCTGCA 120

Qy 958 ccttattaaagaatattgtaagctgtgtagacgtttaaattacacgggtgttcgt 1017

||||| | | | |

Db 121 CCATTAGGAAGAAAGAACTTGAGACACCTGTGAGGCCAAATTTCCTAATGCTAAATTTGGT 180

Qy 1018 caagcctatggttcaacagaacaacctgtgcaattatcatcacacgggaaggcgatga - 1076

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Db 181 CAAAGTTACGAATGACGAAGACCGGACCACTGTTGCTATGCTGCTGGCATTTTGCTAAA 240

Qy 1077 -----taaccgggtgctcttgccaaagtgtgccattttaaagcaaaa 1122

||||| | | | |

Db 241 GAACCCCTTCGAATTAATTAATCTGGAGCATGTGGACCTGTTGTAAGAAATGCTAGATGAAA 300

Qy 1123 gtatcagatctgatataactaaaaaactttggcccgacagacgttggaagtgtgta 1182

||||| | | | |

Db 301 ATTGTGATCTCGTATACCTGCGCAATCTCTCCCTAGAACCAATCTGGAGATTTTGTATA 360

Qy 1183 aaggtctcattgcttataaaggttatagtatgaataaccagaagcaacaagaatacata 1242

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Db 361 ACAGGCGATCAATATGATGAAGGTTACTTAATGATCCAGAGCCACTACGGGAACAATA 420

Qy 1243 gatgaagaaggttggttgacacccagagatattggttatatgaatgaagaagaacattc 1302

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Db 421 GACAAAGAAAGGTGTTACATCGGGCATGATTTGTTATATTGACATCATGATGAGCTT 480

Qy 1303 ttatcgttgatcgtttgaagcttataatcaataacaaagatatcaagttaccactgtc 1362

||||| | | | |

Db 481 TTCATTGTGATCGTTTAAGAATTTGATTAATAATACAAAGATTTCAATGCTCTGCT 540

Qy 1363 gaattagaatctgtctctttgcaacatccaaatatttgatgcgcgcgttgctgctgt 1422

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Db 541 GAACCTGAAGCCCTTCTCTCAATCATCCCAATATTTAGATGCTGCTGTTTCAATG 600

Qy 1423 ccagatccatagctggttgagcttcgcgagctgtgtgtacttaagaagaagaatct 1482

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Db 601 AAAGACGACGACGACGAGGAAGTCTCTGTGCTTTGTTGATGATCAATAGCTCCACA 660

Qy 1483 atgactg 1489

|||||

Db 661 ATTACTG 667

RESULT 4

LOCUS C90519 651 bp mRNA linear EST 20-APR-1998

DEFINITION C90519 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium

ACCESSION C90519

VERSION C90519.1 GI:3060139

KEYWORDS EST.

SOURCE Dictyostelium discoideum.

ORGANISM Dictyostelium discoideum.

Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.

REFERENCE 1 (bases 1 to 651)

AUTHORS Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mita,B.N., Pl.M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochai,H. and Tanaka,Y.

TITLE Developmental cDNA in Dictyostelium discoideum

JOURNAL Unpublished (1998)

COMMENT Contact: Hideko Urushihara

Institute of Biological Sciences

University of Tsukuba

3-3-10 Ten-noda, Tsukuba, Ibaraki 305, Japan

Email: [d402huesakura.cc.tsukuba.ac.jp](mailto:d402huesakura.cc.tsukuba.ac.jp).

FEATURES

source

1. 651

/organism="Dictyostelium discoideum"

/strain="AX4"

/db\_xref="taxon:44689"

/clone="SSI661"

/clone\_id="Dictyostelium discoideum SS (H.Urushihara)"

/dev\_stage="slug"

BASE COUNT 251 a 83 c 110 g 207 t

ORIGIN

Query Match 11.6%; Score 190.4; DB 10; Length 651;

Best Local Similarity 62.6%; Pred. No. 2e-33;

Matches 313; Conservative 0; Mismatches 186; Indels 1; Gaps 1;

Db 1117 gaaagaatcagatctgatataactaaaaaactttggcccgacagacgttggaaggt 1176

||||| | | | |

Db 1 GCTAAATCATCTCTTCACAGACTGTGAGATTTAGGATGATGGTGAAAAGGCTGAATC 60

Qy 1177 ttgttaaggtctcattatgaagaagttatgtatgaataatccagaagcaagaagaa 1236

||||| | | | |

Db	61	TGTATTAAGGTCGCAATGTTATGTTGGTTAT-TATAACAATGAAGAAGCAACCAATGAA	119
QY	1237	atcatagatgaagaaggttggttgcaccacaggagatatgggtlatcagaigaagaataaa	1296
Db	120	GTCATAGATTAAGAATGAGTATCTTTAAAAACGGTGATATGTGGTTAATGTTGAACAAATGCT	179
QY	1297	cattcccttalcogtgaacgtttgaagtcctttaacccaatacaagaagatcatcagta	1356
Db	180	TATTTCTTTATCATCGATATGATCAAAAGCAATTTGATATCAAAAGGTTTCCAAAGTACCA	239
QY	1357	ccgtgcgaatgaagatcctgttccttttgaacacatccaaatattttgaigcgcgcgttgc	1416
Db	240	CCTGCTGATTAAGAGCACTTACTATTATTCATCCAAAGTTGCGAGATGCCGTGTAGTA	299
QY	1417	ggcgcttcagatccatcgtgcgttgaagctccgcggagctgctgttgcacttaagaaga	1476
Db	300	GCTCTTTTAAAAAGGATGATATGGGTAAAGTACCAAGGTTTCGGTGTATTAACAAAAAT	359
QY	1477	aaactatgactgaagaaagaagtaatggtatcagcttgcagtgatccaagtttcaaatgcaaa	1536
Db	360	GAATCTCTTACTGAAAAAAGAACTCTTGGATTTGGGCTCACCCAAAATTTGCCAATTTATATAA	419
QY	1537	cgtttcgcgttgcgtgcgttttgcgttttgcgaagaagtaactaaagtcactatgtaaat	1596
Db	420	CATTTCAGAGGTGGTATCTTTTCATACCTGCATTTCCTAATCTGCAACGTGTAACTA	479
QY	1597	gaacgttaagaacattagaga	1616
Db	480	TTACGTAAAAAATCTTAAAGA	499

RESULT	5
LOCUS	AM621420
DEFINITION	EST312218 tomato root during/after fruit set, Cornell University
ACCESSION	AM621420
VERSION	AM621420.1
KEYWORDS	GI:7333067
SOURCE	EST.
ORGANISM	tomato.
REFERENCE	Lycopersicon esculentum
AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterales; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 582) van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Kochian,L., Liang,F., Hansen,T., Craven,M.B., Bowman,C.L., Rønning,C.M., Niernm,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley S.D. Generation of ESTs from tomato root, during and after fruit set unpublished (1999) Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a> 5 prime sequence.
TITLE	Location/Qualifiers
JOURNAL	1..582
COMMENT	/organism="Lycopersicon esculentum" /cultivar="FA496" /db_xref="taxon:4081" /clone="cLEX11N8" /clone_lib="tomato root during/after fruit set, Cornell University" /tissue_type="root" /dev_stage="plants during and after fruit-set" /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Tanksley; TSK tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."
FEATURES	
source	
BASE COUNT	181 a 99 c 146 g 156 t
ORIGIN	

Query Match	11.5%;	Score 189.8;	DB 9;	Length 582;
Best Local Similarity	60.6%;	Pred. No. 2.7e-33;		
Matches 330;	Conservative 0;	Mismatches 212;	Indels 3;	Gaps 1;

OY	1079	aagcaggcttccttgcgaaagtgtgcccattttaagaacaaagtatcagctcttgata	1138
Db	2	AATCAGGGGCGATTGTGTACCTTTTGAGAGAACGCCAGACTGAATAATTGTGGATCCCGGATA	61
OY	1139	ctaaaaaacattlvggcccgcaacagacgclvlgagaaqtlvtgltaaaagglccatgctta	1198
Db	62	CGGGTTCCTCTCCGCCCGTAACCAACCOCGGGAATTTGCATTGAGGTGATCAAAATCA	121
OY	1199	tgaaggttatgtagataaatccagaagacaagaagaatacatagatgaagaagtttgt	1258
Db	122	TGAAGGTTTACTTGTGATGACCTTGAAAGCTACAGCTAAGAACATTAGAAAAAGAAGATGCT	181
OY	1259	tgcacacagagagatatltggatltaacgatlgaaagaaaacatttcttactgtgacgtt	1318
Db	182	TACACACTGGCGCATWTGGATWTTGATGACGATGATGATGACGTTTTCAICGCGATCGAT	241
OY	1319	tgaagcttctaataataataaagaagatbtcaaagtcaccgttcgaatgaatgclytic	1378
Db	242	TGAAGGAATTGATCAAAATACAAGAGATTTCAAGTGGCGCCTCTGACTCGAAGCACCTTC	301
OY	1379	ttttgcaacatccaataatltttgatlgtccgagcgtlgtcgtlccagatccataagctg	1438
Db	302	TTGTCAACCCACCCCTTAACATTTTCTGATGCTGCTGTGTCCCAATGAAAGATGAACACGG	361
OY	1439	gtgagcttcgcggagcgtlgtfracttaagaagaagaaatctatgactgaataaagaag	1498
Db	362	GAGAGCTTCGATGGCTTTTGTGTAGATCAAATGGATCTCCATTTACTGTAGAGATGAAG	421
OY	1499	taatgattacgtlgtcagtcagttlccaagltgcaaaacglttgcgtgltgltcgtt	1558
Db	422	TGAAGGATTTCTATCTCCAAGCAGTGATATTTCTAATAAGAGAAAT---AAAAGCCTGTATTTT	478
OY	1559	ttgtgacgaagtagtacctaaagtlcacgtgcgtgaanaatlgacgtlaagaagaatlagaaa	1618
Db	479	TGTGTGAGACGGTACCGAATCTCCATCGAAGAAATTTTGAGAAAAGACTTTAAGAGCTA	538
OY	1619	tactg 1623	
Db	539	GACTG 543	
RESULT	6		
LOCUS	A1485586	625 bp mRNA linear EST 18-MAY-2001	
DEFINITION	EST243907 tomato ovary, TMU Lycopersicon esculentum cDNA clone		
ACCESSION	GI485586		
VERSION	A1485586.1		
KEYWORDS	EST.		
SOURCE	Tomato.		
ORGANISM	Lycopersicon esculentum		
REFERENCE	Eukariyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Assteridae; euasterids I; Solanales; Solanaceae; Solanum;		
	Lycopersicon.		
	1 (bases 1 to 625)		
	Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.		
	, Liang,F., Upton,J., Konning,C.M., Graven,M.B., Fujii,C.Y., Bowman,		
	,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley		
	,S.D. and Giovannoni,J.		
	Generation of ESTs from tomato carpel tissue		
	Unpublished (1999)		
TITLE	Contact: CNGI		
JOURNAL	Clemson University Genomics Institute		
COMMENT	Clemson University		
	100 Jordan Hall, Clemson, SC 29634, USA		
	Email: http://www.genome.clemson.edu/orders/index.html.		

FEATURES	Source	Location/Qualifiers
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		/organism="Lycopersicon esculentum"
		/cultivar="TA96"
		/db_xref="taxon:4081"
		/clone="cLED7A3"
		/clone_1lb="tomato ovary, TAMU"
		/tissue_type="carpel"
		/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
		/lab_host="X11-Blue MRF"
		/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; cLED - Tomato Carpel EST Library. OligodT-primed directionally cloned cDNA in vector Lambda Zap II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."
BASE COUNT	197 a	112 c 146 g 169 t 1 others
ORIGIN		
Query Match	11.3%;	Score 185.8; DB 9; Length 625;
Best Local Similarity	58.5%;	Pred. No. 2.3e-32;
Matches 350;	Conservative 0;	Mismatches 233; Indels 15; Gaps 1;
QY	941 ttgcctcggggagacaccttatctcaagaatgtgtgaagctgtgtctagaagttta	1000
DB	18 TTTATGCTGGGGCTCCACCATTTAGGAAAGAACTTGAGACACTGTGAGCCAAATTTC	77
QY	1001 attaccgggtgtctgaagctctgttttaacggaacaacccctgcaatatatca	1060
DB	78 CTAATGCTMAACTTGTCAGAGGTTCAGGAATTCAGAAACCGGACCGACTGTGGCTATGT	137
QY	1061 caccggaa-----ggcgaatgataaaccaacagtgctcttgccaagtgtgc	1105
DB	138 GCTTGGCAATTTCCTAAAGACCCCTCGAAATTAAATTCGAGCATGTGGACTGTGTTA	197
QY	1106 cattattaaagcaaaagtlatcgatccttgatactaaaaaacatttggccgaacagac	1165
DB	198 GAATGCTCAGATGAAATTTGTGATCCTGATCTGACGCAATCTCTCCCTAGAACCAAT	257
QY	1166 gtggagaagttgtgtlaaaggctcctatgcttatgaaagttatgtatataatccagaag	1225
DB	258 CTGGAGAGATTGTGTAAGAGGCGATCAAAATTTATTAAGGTTTAACTTAATGATCCAGAGG	317
QY	1226 caacaagaagaatcatagatgaagaagttgtgtcacacagggagatatgtgtatcag	1285
DB	318 CCACCTACGGGAACATATAGCAAAAGAAAGTGGTTTACATACGGCGATTTGGTTTATTTG	377
QY	1286 atgaagaanaaacatttcttlatcgttgcgtgttgaagtccttlaatcaatacaaaagat	1345
DB	378 ACATGATGATGAGCTTTTCATTGTGGATCGTTTAAAGAAATTTGATTAATTAACAAGAT	437
QY	1346 atcaagatcaccctgtcgtaatatagaatctgttcttlttgcacaatccaaatatlttgatg	1405
DB	438 TTCAATGGGCTCCCTGCTGAACTTGAAGCCCTTCCTCAATCATCCCAATTTTTCAGATG	497
QY	1406 ccggaggtgtgtgtgcgttccagatccctatagctgtgtgagcttccgggaagctgtgtgtac	1465
DB	498 CTGCTGTTGTTTCAATGAAAGCAGCAGCAAGCAGGAGGAAGTTCCTGTGGCTTTGTTGCA	557
QY	1466 ttaagaagaagaatactatgactgaagaagaagaatgatgatcagttgtcgtacgaagt	1523
DB	558 GATCAAAATGGCTCCCAACATTTACTGAAAGTGAAGTCAAAAGATTTCAATACANAGCAGT	615
RESULT	7	
LOCUS	AM218471	
DEFINITION	AM218471	569 bp mRNA linear EST 18-MAY-2001
ACCESSION	AM218471	Lycopersicon esculentum radicle, 5 d post-imbibition, Cornell University
VERSION	AM218471.1	GI:6529345
KEYWORDS	EST.	
SOURCE	tomato.	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
ORGANISM	Lycopersicon esculentum			
	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I: Solanales: Solanaceae: Solanum;			
	Lycopersicon.			
	1 (bases 1 to 569)			
	van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Alm,S., Konning,C.M., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.			
	Generation of ESTs from tomato radicle tissue			
	Unpublished (1999)			
	Contact: CUGI			
	Clemson University Genomics Institute			
	100 Jordan Hall, Clemson, SC 29634, USA			
	Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a>			
	5 prime sequence.			
FEATURES	Location/Qualifiers			
source	1..569			
	/organism="Lycopersicon esculentum"			
	/cultivar="TA496"			
	/db_xref="taxon:4081"			
	/clone="CLE2912"			
	/clone.lib="tomato radicle, 5 d post-imbibition, Cornell University"			
	/tissue.type="radicle"			
	/dev_stage="seedlings 5 days post-imbibition"			
	/note="Vector: pBluescript SK(-); Site_1: EcoRI, Site_2: XhoI, supplier: Tanksley; Tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."			
BASE COUNT	168 a 100 c 148 g 153 t			
ORIGIN				
Query Match	11.1%;	Score 183.2;	DB 9;	Length 569;
Best Local Similarity	62.8%;	Pred. No. 8.9e-32;		
Matches 284;	Conservative 0;	Mismatches 168;	Indels 0;	Gaps 0;
OY 1072	gagtgataaacccaggtgctcttcgcaaaagtctgtgacattatctaagcaaaagtatcgat	1131		
Db 55	GATATTAAATCAGGGGCGATGTGTACCGCTTGTGAGAACGCGAGATGAAATTGTGAT	114		
OY 1132	cttgataactaaaaaaccttgggccgcaagaagcttgagaagcttgtgtlaaagggtcct	1191		
Db 115	CCGGATACGCGTGTCTCTCGCCCGTACCAACCGCGTGAATTGGATTGAGGTGAT	174		
OY 1192	atgcttatagaagggtatctatagataataatccagaagaacaagaagaaatcatagaaga	1251		
Db 175	CAAAATCATGAAAGGTACTTGAATGACCTTGAAAGCTACGCTAGAAACATTAAGAAAAGA	234		
OY 1252	agttgtgtgacacagaagatatattggatatactgaatgaagaagaacattcttatacgt	1311		
Db 235	GGATGTTACACACATGCGCATATTGGATATTATTGACAGATGATGATGAGCTTTTCATCGG	294		
OY 1312	gactgtttgaagctcttlaatacaatacaagaatalcaagataccaacctgtgaatlaga	1371		
Db 295	GATCGATTGAAGGAATTGATCAAAATACAAAGGATTTCAGTGGCGCTGCTGAATCGCA	354		
OY 1372	tctgttcttttgacaatcatcaaatatttttgatgcgagtgctgtcgtgtcccaatcc	1431		
Db 355	GCACCTTCTGTCAACCCACCTTAACATTTCTGATGCTGCTGTGTCCCAATGAAGAATGAA	414		
OY 1432	atagctgtgtgaagcttccgggaagctgtgtgttgaacttaagaagaagaatctatgacga	1491		
Db 415	CAAGCGGGGGAAGTTCCAGTGGCTTTTGTGTTAGATCAAAATGATTCATCCATTACTGAG	474		
OY 1492	aaagaagtatagtattgaattggttgcagtcgaagt 1523			
Db 475	GATGAAGTGAAGATTTCATCTCAAGCAGGT 506			

LOCUS	AI488821	522 bp	mRNA	linear	EST 18-MAY-2000
DEFINITION	EST247160 tomato ovary, TAMU Lycopersicon esculentum cDNA clone				
ACCESSION	AI488821				
VERSION	AI488821.1	GI:4384192			
KEYWORDS	EST.				
SOURCE	tomato.				
ORGANISM	Lycopersicon esculentum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;				
AUTHORS	Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Niernann,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D., and Giovannoni,J.				
TITLE	Generation of ESTs from tomato carpel tissue				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a> .				
FEATURES	Location/Qualifiers				
source	1..522				
	/organism="Lycopersicon esculentum"				
	/cultivar="TA496"				
	/db_xref="taxon:4081"				
	/clone="cLED18L20"				
	/clone_lib="tomato ovary, TAMU"				
	/tissue_type="carpel"				
	/dev_stage="5 days pre-anthesis to 5 days post-anthesis"				
	/lab_host="XL1-Blue MR"				
	/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2: XhoI; cLED - Tomato Carpel EST Library. OligodT-primed directionally cloned cDNA in vector Lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."				
BASE COUNT	156 a 89 c 133 g 144 t				
ORIGIN					
Query Match	11.0%;	Score 181.6;	DB 9;	Length 522;	
Best Local Similarity	62.6%;	Pred. No. 2e-31;			
Matches 283:	Conservative	0;	Mismatches 169;	Indels	0;
				Gaps	0;
0Y	1072 gatgtataaacccgagtgcttcgtgcgaagtgtgcacatttaagaacaaagtatcat	1131			
Db	43 GATATTAAATCAGGGGCGATGTGTACCGTTGTGAGGAACGCAGAGATGAATAATTGTGAT	102			
0Y	1132 ctgtatactataaaaaactttgggcccgcgaacgaagtgtgaagaattgtgtaaaggtcct	1191			
Db	103 CCGGATACGGGTGCTCTCTGCCCCGTAACCAACCGGTGAATTGTGATGTAGAGGTGAT	162			
0Y	1192 atgctatatgaagttatgtagataatccagaagaacaagaagaatctatagatgaaga	1251			
Db	163 CAATATCATGAAGGTTACTTGAATGACCTCGAAGCTACAGACTAGAAACAATAGAAAAAGAA	222			
0Y	1252 ggttggttcacacagagagatatctgggtgtatcagatgtaagaagaaacatttcttatcgtg	1311			
Db	223 GGATGGTTACACACTGCGCATATTGTGATATTATTGACGATGATGATGAGCTTTTCATCGTG	282			
0Y	1312 gatctgttgaagctcttatacaataaagaagatatcaagttaccacctgtgaattagaa	1371			
Db	283 GATTCATTTAAAGAAATTGATCAAAATPCCAAGAAGATTTTCAAGTGCGCTCTGAACCTCGAA	342			
0Y	1372 tctgtctctttcacacatcccaatctttttagtcgcggggttcgctggtccagatcct	1431			
Db	343 GCACCTCTTGTGAACACCACTTAACATTTTGTGATGCTGCTGTGCCAATGAAGAAGTGA	402			
0Y	1432 atagctgtgtgagcttcgcggagcgtgtgttgaacttaagaagaagaatctatgactgaa	1491			

Db	403	CAAGCGGGAGAAAGTTCACGTGGCTTTGTGTGTTAGATCAAAATGAWTACCATTA	CTAG	462
OY	1492	aaagaagtaatgattacgttgtctgctcaagt	1523	
LOCUS				
DEFINITION				
ACCESSION	BE555239	543 bp	MRNA	linear
VERSION	sp87a10.y1	Gm-c1045	Glycine max	cDNA clone
KEYWORDS	Gm-c1045-595 5'	similar to	TR:048868	048868 4-CDUMARATE:COA
SOURCE	2. ; mRNA sequence.			
ORGANISM	BE555239			
	EST.	BE555239.1	GI:9819726	
	soybean.			
	Glycine max			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;			
	Glycine.			
REFERENCE	1 (bases 1 to 543)			
AUTHORS	Shoemaker,R., Keim,P., Vodka,L., Erpelidng,J., Coryell,V., Khanna			
	,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,D., Beck,C.,			
	Wyllie,T., Underwood,K., Steptoe,M., Theislmg,B., Allen,M., Bowers			
	,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk			
	,R., Rittenberg,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann			
	,R., Waterston,R. and Wilson,R.			
TITLE	Public Soybean EST project			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Shoemaker R/Public Soybean EST project			
	Public Soybean EST Project			
	Washington University School of Medicine			
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA			
	Tel: 314 286 1800			
	Fax: 314 286 1810			
	Email: est@watson.wustl.edu			
	This clone is available through: Resgen, Invitrogen Corp. 2130			
	South Memorial Parkway Huntville, AL 35801 For further information			
	call: (800)-533-4363 or contact via email: cdu@resgen.com			
	High quality sequence stop: 416.			
FEATURES	Location/Qualifiers			
source	1..543			
	/organism="Glycine max"			
	/db_xref="taxon:38477"			
	/clone="GENOME SYSTEMS CLONE ID: Gm-c1045-595"			
	/clone_id="Gm-c1045"			
	/issue_type="Hypocotyl, 9-10 day old etiolated seedlings"			
	/lab_host="DH10B"			
	/note="vector: phuescriptII SK+; site.1: EcoRI; site.2:			
	XhoI; This cDNA library was constructed from mRNA isolated			
	from etiolated hypocotyl tissue of 9-10 day old seedlings			
	of the cultivar Williams 82. Complementary DNA was			
	synthesized from mRNA using a primer consisting of a			
	poly(dT) primer with a XhoI restriction site. EcoRI			
	adapters were ligated to the blunt-ended cDNA fragments			
	followed by digestion with EcoRI and XhoI. The cDNA			
	fragments were directionally cloned into the EcoRI-XhoI			
	restriction site of the phuescript vector. The ligated			
	cDNA fragments were transformed into DH10B host cells			
	(Gibco BRL). This library was constructed by Dr. Randy			
	Shoemaker."			
BASE COUNT	184 a	92 c	130 g	137 t
ORIGIN				
Query Match	10.6%;	Score 173.8;	DB 10;	Length 543;
Best Local Similarity	59.0%;	Pred. No. 1.3e-29;		
Matches	317;	Conservative	0;	Mismatches 217; Indels 3; Gaps 1;
OY	1093	ggcaaaagtgtgtccattatlttaagcaaaagttatcgatcttgatactaaaaaacttgg	1152	

Db 7 GGACCGTTGTGAGAAACGCTGAGATGAAATTCGTGATACAGAAACGGGTGATTCACCT 66  
Qy 1153 gcccacagacagcgtggaagattgtgtaaggggtccatctatgaagaattatga 1212  
Db 67 CCAGAAACAAATCCGGAGAAATTTGCATACAGAGGGGCAAGAGTATGAAAGATATCTTA 126  
Qy 1213 gataatccagaagaacagaagaatcatagatgaagaagttgttgacacagagat 1272  
Db 127 AATGACCCAGAGGCTACAGAGAGACTATACAGAGAGAGATGTTACACACAGAGAT 186  
Qy 1273 attggatattcagatgaagaanaacatttcttctatcgttgatcgtttgagcttaac 1332  
Db 187 ATTGTTTCATTTGATGATGATATGATTAAGCTTCATTTGATGATGATGATTAAGATTTGATC 246  
Qy 1333 aatcaagaagatcatcaagaccctgctgattagaatcgttcttcttgaacaatca 1392  
Db 247 AATTCAGAAAGATTTCCAGAGTACCTCTCTGCTGAGCTCGAAAGCTTTGTTGTTCTCACCCA 306  
Qy 1333 aatatattgattgcggcgctgtgctgctccagatccatagctgtgtgagctccggga 1452  
Db 307 AACATTTCTGATGCTGCGCTTGTAGGTATGAAAGATGAAAGCTGCAAGAGAAATTCACATT 366  
Qy 1453 gctgtgtgttactaaagaagaatcctatgactgaaagaagaagtaattgattacgtt 1512  
Db 367 GCATTGTGTTGAAAGCTCAAAATGCTTCTAGAGTTACCGAGGATGAAATTAAGACATACATT 426  
Qy 1513 gctagcaagttcaaatgcaaaacgttgcgtggtgtgctgctgttcttgaagaaga 1572  
Db 427 TCACACACAGGTGATTTTACACAGAGATAGTACAGATTTC--TTCCGAGACTCTATT 483  
Qy 1573 cctaaagttcactgtaaaatgaacgtaagaacatgaagaataatgaagaaga 1629  
Db 484 CCTAAGACACCTCGGCAAAATCTCGGAAAGGATTAACACGAAAGATTAAACGA 540

RESULT 10  
Bg130292 612 bp mRNA linear EST 31-JAN-2001  
LOCUS Bg130292 tomato shoot/meristem Lycopersicon esculentum cDNA clone  
DEFINITION ctoF23J22 5' sequence, mRNA sequence.  
ACCESSION Bg130292  
VERSION Bg130292.1 GI:12630480  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 612)  
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Uterback, T.,  
Hansen, C., Ronning, C. and Tanksley, S.  
Generation of ESTs from tomato shoot/meristem tissue  
Unpublished (2001)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>.  
Location/Qualifiers  
1. 612

FEATURES  
Source

/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="ctof23j22"  
/clone\_lib="tomato shoot/meristem"  
/tissue\_type="shoot/meristem"  
/dev\_stage="developing shoots from 4-6wks old plants"  
/lab\_host="SOLR"  
/note="Vector: plasmid SK(-); Site 1: EcoRI; Site 2:  
XhoI. Small expanding leaves from the growing tip were  
taken from greenhouse plants (4-6wks old TA496). Tissue  
was immediately frozen in liquid nitrogen."

BASE COUNT 189 a 104 c 137 g 182 t  
ORIGIN

Query Match 10.6%; Score 173.6; DB 10; Length 612;  
Best Local Similarity 61.8%; Pred. No. 1.5e-29;  
Matches 294; Conservative 0; Mismatches 179; Indels 3; Gaps 1;

Qy 1148 ctttgagccacagacagcgtggaagttgtgtaaggggtccatctatgaagaatt 1207  
Db 9 CTCTGCCCGGTAAACCAACCGCGGTAATTTGCTTGTAGAGTGTCAATCATGAAAGGTT 68  
Qy 1208 atgataataccagaagaacagaagaatcatagatgaagaagttgttgacacag 1267  
Db 69 ACTTGATATACCTCGTAGAGTACAGCTAGAACATAGAAAAGAGATGGTTACACATG 128  
Qy 1268 gagatattggtattcagatgaagaagaacatttcttctatcgttgatcgtttgaagctt 1327  
Db 129 GCGATTTGTGATATATTTGACGATGATGATGATGATGATGATGATGATGATGATGAT 188  
Qy 1328 taatcaataaagaagatataagatcaagctgctgattagaatctgttcttgaac 1387  
Db 189 TGATCAATATACAAAGGATTTCAAGTGGCGCTGCTGACCTGACGACACTTTGTCAAC 248  
Qy 1388 atcaaatatttgaatgcggcgctgtgctgctccagatccatagctgtgagcttc 1447  
Db 249 ACCCTAATATTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 308  
Qy 1448 cggagcgtgtgttgaatgaagaagaatcctatgactgaaagaagaagaattgatt 1507  
Db 309 CAGTGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 368  
Qy 1508 agttgtcgtcgaagttcaaatgaacaaagcgttgcgtgtgtgtgtgtgtgtgtgtgt 1567  
Db 369 TCATCTCCAGAGAGATGATTTCTATAGAGAAAT--AAAGCGTATATTTTCTGTGAGA 425  
Qy 1568 aagtaacaaagcgtcactgtaaaatgaacgtaagaacatgaagaataactg 1623  
Db 426 CGGTACCGAAATCTCATGAGAAATTTCTGAGAAACACTTAAGAGCTAGACTG 481

RESULT 11  
Bg1923203 606 bp mRNA linear EST 18-OCT-2001  
LOCUS Bg1923203  
DEFINITION EST543107 tomato callus Lycopersicon esculentum cDNA clone  
CLBCT9H20 5' end, mRNA sequence.  
ACCESSION Bg1923203  
VERSION Bg1923203.1 GI:16221846  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 606)  
Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai,  
J., Uterback, T., Van Aken, S., Ronning, C.M., Fraser, C.M., Martin,  
G.B., Tanksley, S.D. and Giovannoni, J.  
Generation of ESTs from tomato callus tissue (2001)  
Unpublished (2001)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>  
This clone is available through the Clemson University Genomics  
Institute  
Seq primer: 73.

FEATURES  
Source

/organism="Lycopersicon esculentum"  
/cultivar="TA496"  
/db\_xref="taxon:4081"  
/clone="clbct9h20"  
/clone\_lib="tomato callus tissue"  
/tissue\_type="callus tissue"  
/dev\_stage="callus tissue from 4-6wks old plants"  
/lab\_host="SOLR"  
/note="Vector: plasmid SK(-); Site 1: EcoRI; Site 2:  
XhoI. Small expanding leaves from the growing tip were  
taken from greenhouse plants (4-6wks old TA496). Tissue  
was immediately frozen in liquid nitrogen."



Db 100 TTGAGACGATTCCTTGACAGA 81

RESULT 13

AL389862 535 bp mRNA linear EST 03-AUG-2000

LOCUS MUBC57H09F1 MUBC Medicago truncatula cDNA clone MUBC57H09 T3, mRNA

DEFINITION sequence.

ACCESSION AL389862

VERSION AL389862.1 GI:3689615

KEYWORDS EST.

ORGANISM barrel medic.

Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

REFERENCE 1 (bases 1 to 535)

AUTHORS Journef,E.P., Crespeau,H., van Tuinen,D., Gouzy,J., Jaillon,O., Niebel,A., Carreau,V., Chataigner,O., Kahn,D., Gianlinazzi-Pearson,V. and Gamas,P.

TITLE Medicago truncatula ESTs from endomycorrhizal roots

JOURNAL Unpublished (2000)

COMMENT Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France

Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr

Contact : Pascal Gamas and Etienne-Pascal Journef, Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : mt-est@toulouse.inra.fr Website : http://sequence.toulouse.inra.fr/Mtruncatula.html).

FEATURES

SOURCE

1. 535

Location/Qualifiers

/organism="Medicago truncatula"

/cultivar="Jemalong"

/db\_xref="taxon:3880"

/clone="MUBC57H09"

/clone\_id="MUBC"

/tissue\_type="arbuscular mycorrhiza"

/dev\_stage="harvested 3 weeks post inoculation with Glomus intraradices"

/note="Vector: pluscript psk; Site\_1: EcoRI; Site\_2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epioses soil : 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LP8 ). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using GigaPack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using Exasit helper phage and propagated in SOBR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note : EST may be of fungal origin."

BASE COUNT 165 a 103 c 124 g 143 t

ORIGIN

Query Match 9.9%; SCORE 162.4; DB: 9; Length 535;

Best Local Similarity 59.6%; Pred. No. 5.4e-27;

Matches 293; Conservative 0; Mismatches 196; Indels 3; Gaps 1;

QY 1115 aagcaaaagtatcgtatgataaaacttggccgcgaacagctgagaag 1174

111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

Db 32 AATCCCAATGTCTGATTGCAACATGCAAGTCCCTTCACCCGATCAATTAGGGGAAA 91

QY 1175 ttgtgtaaaagggtctcattgataaagtgatagataatccagaagaacagaag 1234

111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

Db 92 TTTGGCTACGAGACCTGTTATGATGACAGATFACCTTTAACATCCAGAACAAAC 151

QY 1235 aatcatagatgaagaaggttggtgcacacagagagatacttggttaattacgaaga 1294

111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

Db 152 AAACCATTAATGATCAGGCTTGAGCCCTTACCCGGCATCTTGATATTTGATGAAAAG 211

QY 1295 aacattcttactgctgagcttggaagctcttaataaatacaagaatcaagtac 1354

111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

Db 212 GACACATTATTTGTCGTGATGATGAATAAAGACTCTATCAAGTAAATGGGATTCAGACTGG 271

QY 1355 caactctgaataagaatctgtctctttgcaacatccaataattttgactgcgcgttg 1414

111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

Db 272 CCCCTGCTCACTGCTGAAGACTTACTAATTTTCATCCCTGAATTTCTGATGCCGGGTGA 331

QY 1415 ctggcgttcagatccatagctgctgagcttcgcggagctgttctgtacttaagaag 1474

111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

Db 332 TTCCGCTTCCTCATGCAAGCTGGGAGGTTCCAGTTGCTTTGTTGCTCCTCACTGA 391

QY 1475 gaaatctatgactgaagaagaatgattgactgtctagtcgaagtttcaatgcaa 1534

111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

Db 392 ATAGCTTGATTAACCTGACAGACATCAGAAATTTGTACCAAAAGGTTGCACCTACA 451

QY 1535 aacgttgcgtgtgtgtgtcgttttggagacgaagtaactaaaggtctcactgttaaa 1594

111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

Db 452 AAAGGTGC--GGGAGTGCATTTATAGAGAGATTCCAAAGTCCACCAGCGGAAAGA 508

QY 1595 ttgaaggttaag 1606

111 111 111

Db 509 TTTTAAGAAAG 520

RESULT 14

B1425803 498 bp mRNA linear EST 29-NOV-2001

LOCUS sah72f03.y1 Gm-c1049 glycine max cDNA clone GENOME SYSTEMS CLONE

DEFINITION ID: Gm-c1049-4085 5' similar to TR:048868 048868 4-CODMARATE:COA

IGLISE 2. /, mRNA sequence.

ACCESSION B1425803

VERSION B1425803.1 GI:15203035

KEYWORDS EST.

SOURCE soybean.

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 498)

AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Merritt,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Stepien,B., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shiu,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE Public Soybean EST Project

JOURNAL Unpublished (1999)

COMMENT Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu

This clone is available through: Resgen, Invitrogen Corp, 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccutes@resgen.com High quality sequence stop: 420.

FEATURES

source

1. 498

Location/Qualifiers

/organism="Glycine max"

/db\_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1049-4085"

/clone\_lib="Gm-cl049"  
/tissue\_type="whole seedlings of greenhouse grown plants"  
/dev\_stage="3 week old"  
/lab\_host="DH10B"  
/note="Vector: pBluescript II SK+; Site\_1: EcoRI; Site\_2: XhoI; The Clark NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from whole seedlings of 3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."

BASE COUNT 165 a 86 c 119 g 128 t  
ORIGIN

Query Match 9.9%; Score 162.2; DB 10; Length 498;  
Best Local Similarity 60.5%; Pred. No. 5.9e-27;  
Matches 285; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 1159 aacagacgtggaagaattgtgtaagaggtcctatgtaagaagttatgtagaat 1218  
DB 28 AACAAACACGGTGAATTTGTCATTAAGAGGCACAAAGGTCATGAAGATATCTAAATGAC 87  
QY 1219 ccagaagaacaagaagaatcatagatgaagaagttgtgtgacacagaagatattg 1278  
DB 88 CCAGAGGCTACACAGAGAACTGTAGACCAAGAAGATGTTTACACAGAGATATTGTT 147  
QY 1279 tattacgatgaagaanaaacattcctatcgtagatcggttgaagtttaacaaatc 1338  
DB 148 TTCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 207  
QY 1339 aaagatatcaatgaccacgtgtaattgaattcgttcttttgcacaaatcacaat 1398  
DB 208 AAAGGATTCACAGTGGCTCTGCTGAGCTTGAAGCATTTGTTGATGCCCAACATAT 267  
QY 1399 ttgtatgcggt 1458  
DB 268 TGTGATGCTGCGCTGTGAGCATGAAGAAGATGAGCTGCAAGGAAATTCAGTTGCTTT 327  
QY 1459 gtgtacttaagaagaataatctatgactgaagaagaagtaattgactgttagt 1518  
DB 328 GTTGTAGGTCAAAATGTTCTGAGATCGCCGAGATGAATCAAAATTCATTTCCAA 387  
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## RESULT 15

BG791252

LOCUS BG791252 570 bp mRNA linear EST 16-MAY-2001  
DEFINITION ESTFN1115 Tomato Root Subtraction cDNA Library Lycopersicon  
esculentum cDNA clone 10D1 5' similar to 4-coumarate--CoA ligase 2a  
, mRNA sequence.

ACCESSION

BG791252

VERSION BG791252.1 GI:14126814

KEYWORDS

SOURCE

ORGANISM

Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
Lycopersicon.  
1 (bases 1 to 570)  
AUTHORS Wang, Y.-H., Garvin, D.F. and Koehian, L.V.  
TITLE Nitrate-induced genes in tomato roots: array analysis reveals novel  
genes that may play a role in nitrogen nutrition  
JOURNAL Plant Physiol. 127 (1), 345-359 (2001)  
MEDLINE 21437959  
COMMENT

## CONTACT

Contact: Koehian LV  
US Plant Soil & Nutrition Lab  
Cornell University  
Tower Rd, Ithaca, NY 14853, USA  
Tel: (607) 255-5445  
Fax: (607) 255-1132  
Email: lvk1@cornell.edu  
Seq primer: T3

FEATURES  
source Location/Qualifiers

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/note="Organ: Roots; Vector: pBluescript KS; Directional"  
BASE COUNT 172 a 103 c 136 g 159 t  
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Matches 273; Conservative 0; Mismatches 163; Indels 3; Gaps 1;

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Search completed: September 6, 2002, 17:47:30  
Job time: 9583 sec







GenCore version 4.5  
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## OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 19:27:48 : Search time 5976.93 Seconds  
(without alignments)  
5756.003 Million cell updates/sec

Title: US-09-581-241-5  
Perfect score: 1644  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
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23: em\_pat:\*  
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25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query Match Length DB ID Description

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1644	100.0	1644	6	E36480	E36480 Luciferase	1640.8	99.8	1644	6	E36479	E36479 Luciferase	1636	99.5	1644	6	AR098258	AR098258 Sequence	1636	99.5	1644	6	E02495	E02495 cDNA encodi	1636	99.5	1644	6	E05448	E05448 cDNA sequen	1636	99.5	1781	3	LLUCI	X66919 L. laterali	1628.2	99.0	1908	6	AR043317	AR043317 Sequence	1628.2	99.0	1908	6	AR062709	AR062709 Sequence	1628.2	99.0	1920	6	E16288	E16288 cDNA encodi	1620	98.5	2019	23	E10169	E10169 DNA encodin	1620	98.5	2055	23	E10170	E10170 DNA encodin	1619.6	98.5	1704	6	AR043316	AR043316 Sequence	1619.6	98.5	1704	6	AR062708	AR062708 Sequence	1619.6	98.5	1704	6	E12278	E12278 cDNA encodi	1619.6	98.5	1704	6	E13411	E13411 cDNA encodi	1618.4	98.4	2264	6	E13412	E13412 cDNA encodi	1618.4	98.4	2264	6	AR108849	AR108849 Sequence	1618.4	98.4	2264	6	AR119318	AR119318 Sequence	1618.4	98.4	2264	6	AR151719	AR151719 Sequence	1618.4	98.4	2264	6	AR250561	AR250561 Sequence	1618.4	98.4	2264	6	E01857	E01857 DNA encodin	1618.4	98.4	2264	6	E02267	E02267 cDNA encodi	1618.4	98.4	2264	6	E03259	E03259 cDNA encodi	1618.4	98.4	2264	6	E05447	E05447 cDNA sequen	1618.4	98.4	2264	6	M26194	M26194 Luciola cru	1618.4	98.4	2264	6	AR098254	AR098254 Sequence	1618.4	98.4	2264	6	U49181	U49181 Luciola lat	1618.4	98.4	2264	6	Z4891	Z4891 L. lateralis	1618.4	98.4	2264	6	Z69619	Z69619 L. lateralis	1618.4	98.4	2264	6	U49181	U49181 Luciola lat	1618.4	98.4	2264	6	U51019	U51019 Luciola lat	1618.4	98.4	2264	6	AR098253	AR098253 Sequence	1618.4	98.4	2264	6	AR098255	AR098255 Sequence	1618.4	98.4	2264	6	H0710CT	H0710CT	1618.4	98.4	2264	6	E10030	E10030 cDNA coding	1618.4	98.4	2264	6	S61961	S61961 Luciferase	1618.4	98.4	2264	6	AR89479	AR89479 L. noctiluca	1618.4	98.4	2264	6	AF328553	AF328553 Pyrococli	1618.4	98.4	2264	6	L39928	L39928 Pyrococli	1618.4	98.4	2264	6	X84848	X84848 P. pyralis 1	1618.4	98.4	2264	6	A37556	A37556 Sequence 22	1618.4	98.4	2264	6	AJ277960	AJ277960 Cloning v	1618.4	98.4	2264	6	U02437	U02437 Cloning vec	1618.4	98.4	2264	6	AF093685	AF093685 Luciferas

## ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION Luciferase and method for assaying intracellular ATP by using the same.  
ACCESSION E36480  
VERSION E36480.1 GI:13022687  
KEYWORDS JP 1999239493-A/4.  
SOURCE Luciola lateralis.  
ORGANISM Luciola lateralis  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidae; Lampyridae; Luciola.

REFERENCE 1 (bases 1 to 1644)

AUTHORS Noriaki, H. S. M. M.  
TITLE Luciferase and method for assaying intracellular ATP by using the  
JOURNAL Patent: JP 1999239493-A 4 07-SEP-1999;

COMMENT KIKKOMAN CORP  
OS Luciola lateralis  
PN JP 1999239493-A/4  
PD 07-SEP-1999  
PF 21-DEC-1998 JP 1998363108  
PR

PI	NORIAKI HATTORI, SEIJI MURAKAMI
PC	C12N15/09, C12N9/02, C12Q1/66///C12N9/02, C12R1:19, C12N15/00 CC
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RESULT	2
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LOCUS	E36479 1644 bp DNA linear PAT 07-FEB-2001
DEFINITION	Luciferase and method for assaying intracellular ATP by using the same.
ACCESSION	E36479
VERSION	E36479.1 GI:13022686
KEYWORDS	JP 1999239493-A/3.
SOURCE	Luciola lateralis.
ORGANISM	Luciola lateralis. Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidea; Lampyridae; Luciola.
REFERENCE	1 (bases 1 to 1644)
AUTHORS	Noriaki,H.S.M.M.
TITLE	Luciferase and method for assaying intracellular ATP by using the





COMMENT

RIKMAN CORP  
OS Luciola lateralis  
PN JP 1990171189-A/1  
PD 02-JUL-1998  
PF 22-DEC-1988 JP 1988322029  
PI KAIJIYAMA NAOKI, TATSUMI HIROKI, NAKANO EIICHI PC  
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CC topology: Linear;  
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FH Key Location/Qualifiers  
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FEATURES

Source  
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BASE COUNT 529 a 262 c 349 g 504 t  
ORIGIN

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Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1621 ctgaagaacacagttgtgtgaagtg 1644  
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RESULT 5  
LOCUS E05448 1644 bp RNA linear PAT 29-SEP-1997  
DEFINITION E05448 CDNA sequence of luciferase.  
ACCESSION E05448  
VERSION E05448.1 GI:2173637

KEYWORDS	JP 1993244942-A/2.
SOURCE	Luciola lateralis.
ORGANISM	Luciola lateralis
REFERENCE	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidea; Lampyridae; Luciola.
AUTHORS	1 (bases 1 to 1644)
TITLE	Kajiyama, N. and Nakano, E.
JOURNAL	HEAT-STABLE FIREFLY LUCIFERASE. HEAT-STABLE FIREFLY LUCIFERASE GENE, NEW RECOMBINANT DNA AND PRODUCTION OF HEAT-STABLE FIREFLY LUCIFERASE
COMMENT	Patent: JP 1993244942-A 2 24-SEP-1993; KIRKMAN CORP
FEATURES	OS Luciola lateralis
source	PN JP 1993244942-A/2
	PD 24-SEP-1993
	PF 22-MAY-1992 JP 1992131057
	PR 27-JUN-1991 JP 91P 1571117, 29-NOV-1991 JP 91P 317064 PI
	KAJIYAMA NAOKI, NAKANO EIICHI
	PC C12N9/02,C12N15/53//C12N1/21,(C12N9/02,C12R1:19); CC
	Strandedness: Double;
	CC Topology: Linear;
	CC Hypochemical: No;
	CC anti-sense: No;
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Qy	1141	aaaaaaactcttgagcccgaaacagacgttgtagagaagttgtgtaaaaggtcctatctatg	1200
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Qy	1201	aaaggttatgtagataatccagaagcaacaaagagaatcatatagatgaagaagttggttg	1260
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Qy	1441	gagcttcgggaacgttcttctgaacttaagaagaagaaatctatgaactcgtgaagaagatga	1500
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Qy	1501	atgagattacgtctgtagtcaagtttccaagaatgcaaaacgtttgtcgtgtgtgtcgtcttt	1560
Db	1501	ATGAGATTACGTCTGTAGTCAAGTTTCAATTCGAAAAACGTTTGGCGTGTGTGTCCGTTTT	1560
Qy	1561	gttgcgaaggtacctaagaagctcactcgttlaaattgacggttaagaacaaatagaataa	1620



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LOCUS	L. lateralis luciferase mRNA.		Linear
DEFINITION	X66919.1		INV 24-NOV-1993
ACCESSION	X66919.1		GI:9526
VERSION	X66919.1		GI:9526
KEYWORDS	luciferase.		
SOURCE	Japanese firefly.		
ORGANISM	Lucifera lateralis		
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Phryganea; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidae; Lampyridae; Lucifera.		
REFERENCE	1 (bases 1 to 1781)		
AUTHORS	Tatsumi, H., Kajiyama, N. and Nakano, E.		
TITLE	Molecular cloning and expression in Escherichia coli of a cDNA clone encoding luciferase of a firefly, Lucifera lateralis		
JOURNAL	Biochim. Biophys. Acta 1131 (2), 161-165 (1992)		
MEDLINE	92305054		
REFERENCE	2 (bases 1 to 1781)		
AUTHORS	Tatsumi, H.		
TITLE	Submitted		
JOURNML	Division, Kikkoman Corporation, 399 Noda, Noda City, Chiba 278, JAPAN		
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BASE COUNT	579 a	276 c	367 g
ORIGIN	559 t		
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QY	481	agaagttacaaatccatgacacacttataaaaaaacactccacaaggttccaagga	540
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QY	661	ttctctcaagctagagatccaattatagaaaccaaagttccacgaagccagctattta	720
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## RESULT 7

AR043317

LOCUS AR043317 1908 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 8 from patent US 5814465.

ACCESSION AR043317

VERSION AR043317.1 GI:5964325

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

1 (bases 1 to 1908)

REFERENCE Tatum, H., Fukuda, S., Kikuchi, M. and Koyama, Y.

TITLE Biotinylated firefly luciferase, a gene for biotinylated firefly

luciferase, a recombinant DNA, a process for producing biotinylated

luciferase, and a bioluminescent analysis method

Patent: US 5814465-A 8 29-SEP-1998;

Location/Qualifiers

FEATURES

source

BASE COUNT 598 a 329 c 426 g 555 t

ORIGIN

Query Match 99.0%; Score 1628.2; DB 6; Length 1908;

Best Local Similarity 99.5%; Pred. No. 0;

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 DEFINITION Sequence 8 from patent US 5843746.  
 ACCESSION AR062709  
 VERSION AR062709.1 GI:5990400  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 1908)  
 AUTHORS Tatsumi,H., Fukuda,S., Kikuchi,M. and Koyama,Y.  
 TITLE Biotinates firefly luciferase, a gene for biotinated firefly luciferase, a recombinant DNA, a process for producing biotinated luciferase and a bioluminescent analysis method  
 JOURNAL Patent: US 5843746-A 8 01-DEC-1998;  
 FEATURES  
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 Location/Qualifiers  
 BASE COUNT 598 a 329 c 426 g 555 t  
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 ACCESSION E12279  
 VERSION E12279.1 GI:3251113  
 KEYWORDS JP 1996308578-A/4.  
 SOURCE Luciola lateralis.  
 ORGANISM Luciola lateralis  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
 Elateriformia; Cantharoidea; Lampyridae; Luciola.  
 1 (bases 1 to 1908)  
 Tatum, H., Fukuda, M., Kikuchi, M. and Koyama, T.  
 BIOTIN FIRE FLY LUCIFERASE. BIOTIN FIRE FLY LUCIFERASE GENE, NEW  
 RECOMBINANT DNA, PRODUCTION OF BIOTIN FIRE FLY LUCIFERASE AND  
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 Patent: JP 1996308578-A 4 26-NOV-1996;  
 KIKKOMAN CORP  
 COMMENT  
 OS Luciola lateralis  
 PN JP 1996308578-A/4  
 PD 26-NOV-1996  
 PF 24-APR-1995 JP 1995098857  
 PR 27-JUL-1994 JP 94P 193798, 14-MAR-1995 JP 95P 54625 PI  
 TATSUMI HIROKI, FUKUDA MASARU, KIKUCHI NAMORU, KOYAMA TAJUJI PC  
 C12M15/09, C12M9/02, C12Q1/26, (C12M9/02, C12R1.185); CC  
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lysostaphin.  
ACCESSION E16288  
VERSION E16288.1 GI:5710971  
KEYWORDS JP 1998150991-A/1.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 1920)  
AUTHORS Tatsumi, H., Fukuda, M. and Nagahara, A.  
TITLE LUCIFERASE-LYOSTAPHIN FUSED PROTEIN, ITS PRODUCTION AND  
BIOUMINESCENT ANALYSIS USING THE SAME  
JOURNAL Patient: JP 1998150991-A 1 09-JUN-1998;  
KIKKOMAN CORP  
COMMENT OS None  
OC Artificial sequences.  
PN JP 1998150991-A/1  
PD 09-JUN-1998  
PF 25-NOV-1996 JP 1996328042  
PI TATSUMI HIROKI, FUKUDA MASARU, NAGAHARA AYUMI PC  
C12N15/09,C07H21/04,C07K19/00,C12N9/02,C12N9/52,C12P21/02, PC  
C12Q1/66,  
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CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No;  
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DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)
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DE JP 1995289264-A/1.
XX unclassified.
OS unclassified.
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RP Tatsumi H., Fukuda M.;
RA "VARIANT TYPE STREPTAVIDIN GENE, FUSION PROTEIN GENE OF VARIANT TYPE
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RT PROTEIN OF VARIANT TYPE STREPTAVIDIN-FIREFLY LUCIFERASE";
RL Patent number JP1995289264-A/1, 07-NOV-1995.
RL KIKKOMAN CORP.
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CC OC Artificial sequences.
CC PN JP 1995289264-A/1

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CC PD 07-NOV-1995
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CC CC topology: Linear;
CC CC hypothetical: No;
CC CC anti-sense: No;
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CC FT fusion protein"
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Db 624 CAGTGAAACTGTGAAGAGTCTTTATTCCTGATTAGCCGGTTTATTTATAGTGTCCG 683
Qy 309 tgtgctccaactaatgaattacactctacgtgaattggttcaagtttagagcatc 368
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Db 2004 ACCAGTTGCTAAGATG 2019

RESULT 12  
E10170 standard; DNA; UNC; 2055 BP.  
ID E10170

XX AC E10170;  
XX SV E10170.1  
XX 08-OCT-1997 (Rel. 52, Created)  
DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)  
XX DE DNA encoding mutated streptoavidin-firefly luciferase fusion protein.  
XX KW JP 1995289264-A/2.  
XX OS unidentified.  
XX OC unclassified.  
XX RN [1]  
RP 1-2055  
RA Tatsumi H., Fukuda M.;  
RT "VARIANT TYPE STREPTAVIDIN GENE, FUSION PROTEIN GENE OF VARIANT TYPE  
STREPTAVIDIN-FIREFLY LUCIFERASE, NEW RECOMBINANT AND PRODUCTION OF FUSION  
PROTEIN OF VARIANT TYPE STREPTAVIDIN-FIREFLY LUCIFERASE";  
RL Patent number JP1995289264-A/2, 07-NOV-1995.  
RL KIKKOMAN CORP.  
XX OS None  
CC OC Artificial sequences.  
CC PN JP 1995289264-A/2  
CC PD 07-NOV-1995  
CC PE 27-APR-1994 JP 1994090275  
CC PL TATSUMI H, FUKUDA M, MASARU  
CC PC C12N15/09, C07K14/36, C07K19/00, C12P21/02, G01N33/53, (C12P21/02,  
CC PC C12R1.19);  
CC CC strandedness: Double;  
CC CC topology: Linear;  
CC CC hypothetical: No;  
CC CC anti-sense: No;  
CC CC Key  
CC FH Location/Qualifiers  
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CC FT luciferase fusion  
CC FT protein"  
XX FH Key  
XX FH Location/Qualifiers  
XX FT source  
XX FT 1..2055  
XX FT /db\_xref="taxon:32644"  
XX FT /organism="unidentified"  
XX SQ Sequence 2055 BP; 603 A; 418 C; 474 G; 560 T; 0 other;  
  
Query Match 98.5%; Score 1620; DB 23; Length 2055;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1626; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 249 cagltgaaacgtgaaagatcttcttctcgtatagccggttattttaaagtgctcg 308  
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QY 309 tctgtgtccaaactaagagatttaacactctagtcgtgaatttggttcaagtttaagcatctc 368  
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Db 720 TGTGGCTCCAACTAATGAGATTTTACACTGACTGGAATTTGGTTCAAGTTTAAAGCATCTC 779  
QY 369 taagcaacaattgtatlltagttcttaaaaaaggattagataagttataactcttacaana 428  
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QY 429 aacggttaactgcbatataaaccatgttattatgtgaacgaagttgattatagaagttta 488  
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QY 489 tcaatccatgagacaacttattataaaaaaacactccacaaggttccaagaatcgaattc 548  
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Db 960 TAAACTGTAGAGTTTAACCGCAAGACAGAGTGGCTCTTATATAGAACTCTTCGGGTTTC 1019  
QY 609 aacgggtttgcaaaaagtggtgcaacttactactcaatgaataatcgtcaatagatttctca 668  
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QY 669 cgttagagatccaattatagaaaccaaagtttcaacgaagcaggtattttaactgtagt 728  
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QY 729 accattccatcagttgttggatagtttactacttaaggtctactactgttggtttcg 788  
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Db 1140 ACCATTCCATCATGGTTTGGTATGTTTACTTATTAAGCTATCTTAACCTTGCTGTTTTCG 1199  
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Db 1800 TCCAAATATTTTGTATGTCGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1859  
QY 1449 gggagctgt 1508  
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Db 1860 GGGAGCTGT 1919  
QY 1509 cgttgcagtagcaagtttcaaaatgcaaaagcgttgcgtgtgtgtgtgtgtgtgtgtgt 1568  
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Db 1920 CGTTGCTAGTCAAGTTTCAAAATGCAAAACGTTTGCCTGTGTGTGTGTGTGTGTGTGTGT 1979  
QY 1569 agtacttaaaaggtctcaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1628  
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Db 1980 AGTACCTAAAGGTCTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2039  
QY 1629 accagttgctgaagtg 1644  
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Db 2040 ACCAGTTGCTAAGATG 2055

RESULT 13  
AR043316  
LOCUS AR043316 1704 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 5 from patent US 5814465.  
ACCESSION AR043316  
VERSION AR043316.1 GI:5964324  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1704)  
AUTHORS Tatsumi,H., Fukuda,S., Kikuchi,M. and Koyama,Y.  
TITLE Biotinlated firefly luciferase, a gene for biotinated firefly luciferase, a recombinant DNA, a process for producing biotinated luciferase and a biooluminescent analysis method  
JOURNAL Patent: US 5814465-A 5 29-SEP-1998;  
FEATURES  
source Location/Qualifiers  
BASE COUNT 541 a 275 c 361 g 527 t  
ORIGIN  
Query Match 98.5%; Score 1619.6; DB 6; Length 1704;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1625; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
QY 11 tggagaagcatgaaatattgtatggttccgtgaaccatttaccctattgaagaagat 70  
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RESULT 14  
AR062708  
LOCUS AR062708 1704 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 5 from patent US 5843746.  
ACCESSION AR062708  
VERSION AR062708.1 GI:5990399  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1704)  
AUTHORS Tatsumi,H., Fukuda,S., Kikuchi,M. and Koyama,Y.  
TITLE Biotinlated firefly luciferase, a gene for biotinlated firefly luciferase, a recombinant DNA, a process for producing biotinlated luciferase, and a bioluminescent analysis method  
JOURNAL Patent: US 5843746-A 5 01-DEC-1996;  
FEATURES  
source Location/Qualifiers  
BASE COUNT 541 a 275 c 361 g 527 t  
ORIGIN

Query Match 98.5%; Score 1619.6; DB 6; Length 1704;  
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 DEFINITION CDNA encoding biotinylated Luciola luciferase.  
 ACCESSION E12278  
 VERSION E12278.1 GI:3251112  
 KEYWORDS JP 1996308578-A/3.  
 SOURCE  
 ORGANISM  
 Luciola lateralis  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
 Elateriformia; Cantharoidae; Lampyridae; Luciola.  
 REFERENCE  
 AUTHORS Tatsumi, H., Fukuda, M., Kikuchi, M. and Koyama, T.  
 TITLE 1 (bases 1 to 1704)  
 BIOTIN FIRE FLY LUCIFERASE. BIOTIN FIRE FLY LUCIFERASE GENE, NEW  
 RECOMBINANT DNA, PRODUCTION OF BIOTIN FIRE FLY LUCIFERASE AND  
 BIOLUMINESCENCE ANALYSIS  
 Patent: JP 1996308578-A 3 26-NOV-1996;  
 KIKKOMAN CORP  
 JOURNAL  
 COMMENT  
 OS Luciola lateralis  
 PN JP 1996308578-A/3  
 PD 26-NOV-1996  
 PF 24-APR-1995 JP 1995098857  
 PR 27-JUL-1994 JP 94P 193798, 14-MAR-1995 JP 95P 54625 PI  
 TATSUMI H, FUKUDA MASARU, KIKUCHI MAMORU, KOYAMA TAJUJI PC  
 C12N15/09, C12N9/02, C12Q1/26, (C12N9/02, C12R1:185); CC  
 strandedness: Double;  
 CC topology: Unknown;  
 CC hypothetical: No;  
 CC anti-sense: No;  
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 FT mat\_peptide 1..1704  
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 /db\_xref='taxon:7052'  
 BASE COUNT 541 a 275 c 361 g 527 t  
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 Best Local Similarity 99.4%; Pred. No. 0;  
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 Db 1691 CAGTTGCTAAGATG 1704

Search completed: September 6, 2002, 19:28:23  
 Job time: 15466 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 19:38:41 : Search time 512.01 Seconds  
(without alignments)  
5512.797 Million cell updates/sec

Title: US-09-581-241-5  
Perfect score: 1644  
Sequence: 1 atggaacaatcgtggaacga.....agaacacagtgtcaatgatg 1644

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
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3: /SID55/gcgcdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
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5: /SID55/gcgcdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1644	100.0	1644	20	AAx84396
2	1640.8	99.8	1644	20	AAx84395
3	1636	99.5	1644	14	AAO34745
4	1632.8	99.3	1644	11	AAO325718
5	1628.2	99.0	1644	18	AAO325718
6	1628.2	99.0	1644	11	AAO325718
7	1620	98.5	1620	17	AAx3850
8	1620	98.5	1620	17	AAx3851
9	1620	98.5	1620	17	AAx3851

10	1619.6	98.5	1704	18	AAx63268
11	1619.6	98.5	1704	19	AAx23595
12	1618.4	98.4	2364	19	AAx23580
13	1490.4	90.7	1656	20	AAx25717
14	1357.6	82.6	1644	10	AAx91170
15	1357.6	82.6	1644	11	AAO03801
16	1357.6	82.6	1644	12	AAO13844
17	1357.6	82.6	1644	22	AAO22186
18	1357.6	82.6	1644	22	AAO22186
19	1356	82.5	1644	12	AAO33825
20	1356	82.5	1644	14	AAO34987
21	1354.4	82.4	1644	12	AAO13840
22	1354.4	82.4	1644	12	AAO13841
23	1354.4	82.4	1644	12	AAO13842
24	1354.4	82.4	1644	12	AAO13843
25	1354.4	82.4	1644	12	AAO13845
26	1264.8	76.9	1656	20	AAx25716
27	1042.4	63.4	1656	20	AAx25715
28	1016	61.8	1970	16	AAO0613
29	750	45.6	10533	16	AAO98930
30	750	45.6	10558	16	AAO98912
31	749.6	45.6	6565	22	AAx5126
32	749.6	45.6	6971	22	AAx5124
33	749.6	45.6	7558	22	AAx5125
34	749.6	45.6	7969	22	AAx5123
35	747.4	45.5	5427	22	AAx83390
36	746.8	45.4	1811	15	AAO58732
37	746.8	45.4	5620	18	AAx48630
38	746.8	45.4	5620	22	AAx30233
39	746.8	45.4	5789	20	AAx08779
40	746.8	45.4	5791	20	AAx08778
41	746.8	45.4	5793	20	AAx08776
42	746.8	45.4	5793	20	AAx08777
43	746.8	45.4	5818	21	AAx38352
44	746.8	45.4	5819	20	AAx08775
45	746.8	45.4	5819	20	AAx08774

#### ALIGNMENTS

RESULT 1  
ID AAx84396 standard; DNA; 1644 BP.  
XX AAx84396;  
AC  
XX 09-SEP-1999 (first entry)  
DT  
XX L. lateralis luciferase coding sequence.  
DE  
XX  
KW Luciferase; surfactant-tolerant; firefly; intracellular ATP assay; ss.  
OS Luciola lateralis.  
XX  
XX WO9933997-A1.  
PN  
XX  
XX 08-JUL-1999.  
PD  
XX  
XX 24-DEC-1998; 98WO-JP05864.  
PF  
XX 26-DEC-1997; 97JP-0361022.  
PR  
XX  
XX (KIKK) KIKKOMAN CORP.  
PA  
XX Hattori N, Murakami S;  
XX WPI; 1999-419109/35.  
XX P-PSDB; AAx22183.  
XX Modified luciferase tolerant to surfactants and useful for assay of  
PT Intracellular ATP  
XX

PS Example 2; Page 43-48; 56pp; English.

CC This sequence encodes a *Luciola lateralis* luciferase of the invention.  
CC The protein is a surfactant-tolerant luciferase which is derived from  
CC firefly luciferase by replacement of the glutamic acid residue at  
CC position 490 by another amino acid. The luciferase can be used in an  
CC assay of intracellular ATP in biological samples containing cells, for  
CC example for establishing the presence of cells, and their quantity, in  
CC the sample. The method can be applied to foodstuffs, drugs,  
CC agrochemicals, beverages and environmental samples. The activity of the  
CC surfactant-tolerant luciferase is not lowered by the presence of high  
CC concentrations of surfactant and therefore an assay of high accuracy can  
CC be carried out in a simple manner

Sequence 1644 BP; 529 A; 262 C; 348 G; 505 T; 0 other;

Query Match	100.0%	Score 1644;	DB 20;	Length 1644;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1644; Conservative	0;	Mismatches	0;	Indels 0; Caps 0;

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QY	61	gaagagggatctcgtctggagccaactctgcgcgaagtatactgatactgcaaaacttga	120
Db	61	gaagagggatctcgtctggagccaactctgcgcgaagtatactgatactgcaaaacttga	120
QY	121	gcaattgcttttacttaacgcacctaaccggtgtcgcatactacgtacgcgcgaatactta	180
Db	121	gcaattgcttttacttaacgcacctaaccggtgtcgcatactacgtacgcgcgaatactta	180
QY	181	aaatcattcctctcaggagagagcgtttaaagaattatggttttggtttgtagaagaatt	240
Db	181	aaatcattcctctcaggagagagcgtttaaagaattatggttttggtttgtagaagaatt	240
QY	241	gcgttatctgcaatgtaaaactgtgaagaattctttatcttcctgatatagccggtttatta	300
Db	241	gcgttatctgcaatgtaaaactgtgaagaattctttatcttcctgatatagccggtttatta	300
QY	301	gggtctcggtgtgtgcctcaactaatlgagatctaacctctacgcgtgaattgtgttcaagtt	360
Db	301	gggtctcggtgtgtgcctcaactaatlgagatctaacctctacgcgtgaattgtgttcaagtt	360
QY	361	ggcctctcttaagcccaaaatctgtatgaagttcttaaaaaagaattagataaagttataact	420
Db	361	ggcctctcttaagcccaaaatctgtatgaagttcttaaaaaagaattagataaagttataact	420
QY	421	gtacaaaaaaacggtacactgtctattaaacaattgttatacttgagcagcaagtggtat	480
Db	421	gtacaaaaaaacggtacactgtctattaaacaattgttatacttgagcagcaagtggtat	480
QY	481	agaggttatcaatccatctgtagacaactttatataaaaaaacatccacaaagttccaagga	540
Db	481	agaggttatcaatccatctgtagacaactttatataaaaaaacatccacaaagttccaagga	540
QY	541	tcaagttttaaaactctgtatagaagtttaacccgcaaaagaacaagttgcctttaaagaactc	600
Db	541	tcaagttttaaaactctgtatagaagtttaacccgcaaaagaacaagttgcctttaaagaactc	600
QY	601	tccggttccaacccggtttgcccacaaagtggtgcaacttactctatgaanaatatcgctactga	660
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QY	661	ttttctcaacgtctagatccaatttatgaaacccaagtttcaccagcagcagctatttta	720
Db	661	ttttctcaacgtctagatccaatttatgaaacccaagtttcaccagcagcagctatttta	720
QY	721	actgtatgacattccatctatgtgtttgtgtatgtttactactttagctatcttaactgt	780
Db	721	actgtatgacattccatctatgtgtttgtgtatgtttactactttagctatcttaactgt	780

QY	781	ggcttcglatgcatggttaacgaaatcttgacgaagaagcctttttaaaacactgcga	840
Db	781	ggcttcglatgcatggttaacgaaatcttgacgaagaagcctttttaaaacactgcga	840
QY	841	gattcaaatgttcaagcggtatctctgtacacgcacttggttgcaattcttaataagat	900
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QY	901	gaattactcgcataatatgatatttacaatttagttgaatctgcactcgcgcgaacct	960
Db	901	gaattactcgcataatatgatatttacaatttagttgaatctgcactcgcgcgaacct	960
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QY	1081	ccagtgcttcttgccaagtgtgcacattttaagcaaaatttcgatcttgatct	1140
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QY	1141	aaaaaactcttggcccgcaacagacgcgtggaagaattgtgttaaaagggtccatgcatatg	1200
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Db	1321	aagttcttaatcaataacaaagatatcaagtaaccacctgcgtgaattagaatcgttctt	1380
QY	1381	ttgcaaacatccaataatttttgaatgcgcgctgttcgttgcgttccagaatccatagctgtg	1440
Db	1381	ttgcaaacatccaataatttttgaatgcgcgctgttcgttgcgttccagaatccatagctgtg	1440
QY	1441	gagcttcgggagagctgtgttctgtacttaagaagaagaatactatgacttgaaaaagaagta	1500
Db	1441	gagcttcgggagagctgtgttctgtacttaagaagaagaatactatgacttgaaaaagaagta	1500
QY	1501	atgattatcgttctgtagtcaagttccaatctgcaaaacgcttgcgtggtgttcgcttt	1560
Db	1501	atgattatcgttctgtagtcaagttccaatctgcaaaacgcttgcgtggtgtgttcgcttt	1560
QY	1561	gttgagcagagacttaagaagctctcaacgtgtaaaatttgacgttaagaacgaattagagaata	1620
Db	1561	gttgagcagagacttaagaagctctcaacgtgtaaaatttgacgttaagaacgaattagagaata	1620
QY	1621	ctgaagaacaaccagttgcataagatg	1644
Db	1621	ctgaagaacaaccagttgcataagatg	1644
RESUL.T 2			
AAx84395			
ID AAx84395 standard, DNA; 1644 BP.			
AAx84395:			
AC			
XX			
DT 09-SEP-1999 (first entry)			
XX			
DE L. lateralis luciferase coding sequence.			
XX			
XX Luciferase; surfactant-tolerant; firefly; intracellular ATP assay; ss			

OS Luciola lateralis.  
 XX MO9933997-A1.  
 XX  
 PD 08-JUL-1999.  
 XX  
 PF 24-DEC-1998; 98MO-JP05864.  
 XX  
 PR 26-DEC-1997; 97JP-0361022.  
 XX  
 PA (KIKK ) KIKKOMAN CORP.  
 XX  
 PI Hattori N, Murakami S;  
 XX  
 XX WPI: 1999-419109/35.  
 DR P-PSDB; AAY22182.  
 XX  
 PT Modified luciferase tolerant to surfactants and useful for assay of  
 intracellular ATP  
 XX  
 PS Example 2: Page 34-39; 56pp; English.  
 XX  
 CC This sequence encodes a Luciola lateralis luciferase of the invention.  
 CC The protein is a surfactant-tolerant luciferase which is derived from  
 CC firefly luciferase by replacement of the glutamic acid residue at  
 CC position 490 by another amino acid. The luciferase can be used in an  
 CC assay of intracellular ATP in biological samples containing cells, for  
 CC example for establishing the presence of cells, and their quantity, in  
 CC the sample. The method can be applied to foodstuffs, drugs,  
 CC agrochemicals, beverages and environmental samples. The activity of the  
 CC surfactant-tolerant luciferase is not lowered by the presence of high  
 CC concentrations of surfactant and therefore an assay of high accuracy can  
 CC be carried out in a simple manner.  
 XX  
 SQ Sequence 1644 BP: 528 A; 261 C; 349 G; 506 T; 0 other;

Query Match 99.8%; Score 1640.8; DB 20; Length 1644;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1644; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atggaacacatgaggaacagatgataatgtgtatgtgtcctggaacatttaccatt 60  
 Db 1 atggaacacatgaggaacagatgataatgtgtatgtgtcctggaacatttaccatt 60  
 QY 61 gaagagagatctgtgagagacaaatgagcaatgataatgataatgcaaaacttga 120  
 Db 61 gaagagagatctgtgagagacaaatgagcaatgataatgataatgcaaaacttga 120  
 QY 121 gcaattgcttacttaacgacacttaacgagtgatatacgtacgacgaacttga 180  
 Db 121 gcaattgcttacttaacgacacttaacgagtgatatacgtacgacgaacttga 180  
 QY 181 aaatcatgctgtctagagagagcttaagaatattgtgtgtgtgtatgagagaat 240  
 Db 181 aaatcatgctgtctagagagagcttaagaatattgtgtgtgtgtatgagagaat 240  
 QY 241 ggtttatgcaatgaaactgtgaagaattcttatttctgtatgaacgcgtttattata 300  
 Db 241 ggtttatgcaatgaaactgtgaagaattcttatttctgtatgaacgcgtttattata 300  
 QY 301 ggtgtcgtgtgctcacaactatgagatttactactcactcagtgatattgttcaagttta 360  
 Db 301 ggtgtcgtgtgctcacaactatgagatttactactcactcagtgatattgttcaagttta 360  
 QY 361 ggcattcttaagcacaactatgattttagtcttaaaaaagattagataaagtattact 420  
 Db 361 ggcattcttaagcacaactatgattttagtcttaaaaaagattagataaagtattact 420  
 QY 421 gtacaaaaaacgttaacgtctataaacattgttatattgagcagaagaatgattat 480  
 Db 421 gtacaaaaaacgttaacgtctataaacattgttatattgagcagaagaatgattat 480

QY 481 agaggtatcaatccatgagcaacttattaaaaaacctccacaaagtttcaaga 540  
 Db 481 agaggtatcaatccatgagcaacttattaaaaaacctccacaaagtttcaaga 540  
 QY 541 tcaagttttaaactgttagaagtttaacgcgaagaacaaagttgtcttataatgaact 600  
 Db 541 tcaagttttaaactgttagaagtttaacgcgaagaacaaagttgtcttataatgaact 600  
 QY 601 tgggttcaacccggtttgccaagaagtgtagcaacttaccatgaanaatctgactaga 660  
 Db 601 tgggttcaacccggtttgccaagaagtgtagcaacttaccatgaanaatctgactaga 660  
 QY 661 ttctccacgttagagatccaattttagaagaacaaagtttccacgagcgacttatta 720  
 Db 661 ttctccacgttagagatccaattttagaagaacaaagtttccacgagcgacttatta 720  
 QY 721 actgtatgaacattccatcatggtttgtatgttacttactttaggtatctactgt 780  
 Db 721 actgtatgaacattccatcatggtttgtatgttacttactttaggtatctactgt 780  
 QY 781 ggtttcgtatgttcatgtttagcgaattttagcgaagaagactttttaaactctgca 840  
 Db 781 ggtttcgtatgttcatgtttagcgaattttagcgaagaagactttttaaactctgca 840  
 QY 841 gattacaatgttcaagcgcttattctgtacccgacttgttgcgaatttcttaagaagt 900  
 Db 841 gattacaatgttcaagcgcttattctgtacccgacttgttgcgaatttcttaagaagt 900  
 QY 901 gaattcctcgataaataatgattatcaaatagttgaattgcaatgcatcggcgagacact 960  
 Db 901 gaattcctcgataaataatgattatcaaatagttgaattgcaatgcatcggcgagacact 960  
 QY 961 ttatcctaaagaatgttgaagctgtgtgttagaagtttgaatccgggttgcgtca 1020  
 Db 961 ttatcctaaagaatgttgaagctgtgtgttagaagtttgaatccgggttgcgtca 1020  
 QY 1021 ggtatgtgtttaaagaaacaaactctgcgaatattatcacacgggaagcgatgataa 1080  
 Db 1021 ggtatgtgtttaaagaaacaaactctgcgaatattatcacacgggaagcgatgataa 1080  
 QY 1081 ccaggtgtcttgcgaagttgtgcatattttaaagcaaaagtatcgcattcgatct 1140  
 Db 1081 ccaggtgtcttgcgaagttgtgcatattttaaagcaaaagtatcgcattcgatct 1140  
 QY 1141 aaaaaaacttggcccggaacagctgggaagaattgtgtgaagaagtcctatgtctatg 1200  
 Db 1141 aaaaaaacttggcccggaacagctgggaagaattgtgtgaagaagtcctatgtctatg 1200  
 QY 1201 aaaggtatgtatgataatccagaagcaacagaagaatcatagatgaagaagttgtgt 1260  
 Db 1201 aaaggtatgtatgataatccagaagcaacagaagaatcatagatgaagaagttgtgt 1260  
 QY 1261 cacacagagatatgtgtgtatcagatgaagaagaacattcttcttctgtgacgtttg 1320  
 Db 1261 cacacagagatatgtgtgtatcagatgaagaagaacattcttcttctgtgacgtttg 1320  
 QY 1321 aagttctttaaatacaagaagatatcaagttacacacgcgttggaattgaacatcgttct 1380  
 Db 1321 aagttctttaaatacaagaagatatcaagttacacacgcgttggaattgaacatcgttct 1380  
 QY 1381 ttgcaacatccaataattttttagtcgcgggtgtgtcgtgcttcagatccatagctgtg 1440  
 Db 1381 ttgcaacatccaataattttttagtcgcgggtgtgtcgtgcttcagatccatagctgtg 1440  
 QY 1441 gaagttccgggaagctgtgtgttacttaagaagaagaatctatgactgaagaagta 1500  
 Db 1441 gaagttccgggaagctgtgtgttacttaagaagaagaatctatgactgaagaagta 1500  
 QY 1501 atggaatcgttgcagtcgaagtttcaaatgcaaaagcttgcgtgtgtgtgtcgtttt 1560  
 Db 1501 atggaatcgttgcagtcgaagtttcaaatgcaaaagcttgcgtgtgtgtgtcgtttt 1560  
 QY 1561 gtgagcgaagttacttaagaagttcactgttlaaaattgacgtgaagaacttagagaata 1620

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Db 1561 gtgagcagaagtaacctaaagctcactcgttaaatgacgtgaagaactttagaata 1620
OY 1621 ctgaagaacacagctgtcgaagtg 1644
    |||||||
Db 1621 ctgaagaacacagctgtcgaagtg 1644

RESULT 3
AA034745
ID AA034745 standard; cDNA to mRNA; 1644 BP.
XX
AC AA034745;
XX
DT 24-MAY-1993 (first entry)
XX
DE Thermostable luciferase (wild-type).
XX
KW Firefly; Luciola cruciata; GENJI; Luciola lateralis; HEIKE;
  mutant; assay; ss.
XX
OS Luciola lateralis.
XX
PN EP524448-A.
XX
PD 27-JAN-1993.
XX
PE 26-JUN-1992; 92EP-0110808.
XX
PR 27-JUN-1991; 91JP-0157117.
PR 29-NOV-1991; 91JP-0317064.
PR 22-MAY-1992; 92JP-0131057.
XX
PA (KIKK ) KIKKOMAN CORP.
XX
PI Elitchi N, Naoki K:
XX
DR MPI: 1993-028553/04.
DR P-PSDB: AAR30803.
XX
PT New DNA sequence of a thermostable luciferase - has the aminoacid
  at position 217 of Luciola cruciata or lateralis luciferase
  replaced by a hydrophobic aminoacid
XX
PS Claim 1-3; Page 29-30 + 21-24; 33pp; English.
XX
CC A DNA sequence of a thermostable luciferase of a firefly, which
  encodes the amino acid sequence of a wild-type firefly luciferase in
  which an amino acid at the 217 position or an amino acid at the
  cruciata equiv. to the 217 position of the luciferase of Luciola
  cruciata (GENJI firefly) of Luciola lateralis (HEIKE firefly) is
  replaced by a hydrophobic amino acids, esp. Ile, Leu or Val, is
  claimed. The mutant luciferase is identical in properties to the
  wild-type luciferase except that it is stable when heated to high
  temps., e.g. 50 degrees C. The luciferase can be used in assays for
  e.g. ATP.
XX
SQ Sequence 1644 BP; 529 A; 262 C; 349 G; 504 T; 0 other;

Query Match 99.5%; Score 1636; DB 14; Length 1644;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 atggaacaacatggaacacatgtaataatgtgtatgtgctcgaacatttaccctatt 60
    |||||||
Db 1 atggaacaacatggaacacatgtaataatgtgtatgtgctcgaacatttaccctatt 60

OY 61 gaagagagatctgctggaacaaatgycgaagatatagtatcgatatagcgaacttga 120
    |||||||
Db 61 gaagagagatctgctggaacaaatgycgaagatatagtatcgatatagcgaacttga 120

OY 121 gcaatgtcttacttaacgaactacgcgtgtcgattatacgttaacgcgaactttagaa 180
    |||||||
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Db 121 gcaatgtcttacttaacgaactacgcgtgtcgattatacgttaacgcgaactttagaa 180
OY 181 aaatactctgtctagagaagccttaagaattatggttggtgtgtatggaagatt 240
    |||||||
Db 181 aaatactctgtctagagaagccttaagaattatggttggtgtgtatggaagatt 240

OY 241 gcgttatgcagtgaagaacagtgaagaattccttatccgttatgaacgggtttattata 300
    |||||||
Db 241 gcgttatgcagtgaagaacagtgaagaattccttatccgttatgaacgggtttattata 300

OY 301 ggtgtcgtgtgtgctcccaactatgagattacactctacgtgaattggttcacagtta 360
    |||||||
Db 301 ggtgtcgtgtgtgctcccaactatgagattacactctacgtgaattggttcacagtta 360

OY 361 ggcattctcaagcccaacattgtattagtctctaaaaagagattagataaattact 420
    |||||||
Db 361 ggcattctcaagcccaacattgtattagtctctaaaaagagattagataaattact 420

OY 421 gtacaaaaaagcgttaactcttaaaaccattgtattatgtgacagcaagtgattat 480
    |||||||
Db 421 gtacaaaaaagcgttaactcttaaaaccattgtattatgtgacagcaagtgattat 480

OY 481 agaggttatcaatccatggaacactttataaaaaaacactccaaggttccaaga 540
    |||||||
Db 481 agaggttatcaatccatggaacactttataaaaaaacactccaaggttccaaga 540

OY 541 tcaagttttaaactgttagaagttaacgcgaagaacaaagtgtcttataatgaact 600
    |||||||
Db 541 tcaagttttaaactgttagaagttaacgcgaagaacaaagtgtcttataatgaact 600

OY 601 tcaagttttaaactgttagaagttaacgcgaagaacaaagtgtcttataatgaact 600
    |||||||
Db 601 tcaagttttaaactgttagaagttaacgcgaagaacaaagtgtcttataatgaact 600

OY 601 tcaagttttaaactgttagaagttaacgcgaagaacaaagtgtcttataatgaact 600
    |||||||
Db 601 tcaagttttaaactgttagaagttaacgcgaagaacaaagtgtcttataatgaact 600

OY 661 tttctcagctagaagatccaatttatgtgaaacccaagttccacagcaggttatta 720
    |||||||
Db 661 tttctcagctagaagatccaatttatgtgaaacccaagttccacagcaggttatta 720

OY 721 actgtatgataccattccatcatatggtttgtatggttactactttagtctattactgt 780
    |||||||
Db 721 actgtatgataccattccatcatatggtttgtatggttactactttagtctattactgt 780

OY 781 ggtttcgatgtcatgtttaacgaatttgacgaagaagactttttaaacactgtcaa 840
    |||||||
Db 781 ggtttcgatgtcatgtttaacgaatttgacgaagaagactttttaaacactgtcaa 840

OY 841 gattacaacatgttcaagcgttattctgttacccagctgtgttgaactcttaataaga 900
    |||||||
Db 841 gattacaacatgttcaagcgttattctgttacccagctgtgttgaactcttaataaga 900

OY 901 gaattaccgtaaaatgatattatcaaatattagttgaattgcatctggcggaagcact 960
    |||||||
Db 901 gaattaccgtaaaatgatattatcaaatattagttgaattgcatctggcggaagcact 960

OY 961 ttatctaagaanaatgtgtgaagctgtgtgtagagcgttttaatttaccggtgtgtcga 1020
    |||||||
Db 961 ttatctaagaanaatgtgtgaagctgtgtgtagagcgttttaatttaccggtgtgtcga 1020

OY 1021 ggtctatggtttaacagaacaaactctgtcaattatcatcaacgcgaagcgatgataa 1080
    |||||||
Db 1021 ggtctatggtttaacagaacaaactctgtcaattatcatcaacgcgaagcgatgataa 1080

OY 1081 ccaagtgctcttcggaaggtgtgtgcattattttaagaagaagttatcgacttgaact 1140
    |||||||
Db 1081 ccaagtgctcttcggaaggtgtgtgcattattttaagaagaagttatcgacttgaact 1140

OY 1141 aaaaaaactttggtgcccgaacagacgttggagaagtttgtataaaggtcctatgctatg 1200
    |||||||
Db 1141 aaaaaaactttggtgcccgaacagacgttggagaagtttgtataaaggtcctatgctatg 1200

OY 1201 aaagttatgtatagataatccagaagcaacaagaagaatcatatagatgaagaagttgtgt 1260
    |||||||
```



Db 1201 aaaggtatgtagataatccagaagcaacagagaataatcatalgtaagaaagtgtgtg 1260  
 Qy 1261 caccacagagatattgggtattacgatgaagaaacattcttatcgtagatcgttg 1320  
 Db 1261 caccacagagatattgggtattacgatgaagaaacattcttatcgtagatcgttg 1320  
 Qy 1321 aagctttaaatacaatacaagaatatacaagtaacacccgtctgaattagaatctgttct 1380  
 Db 1321 aagctttaaatacaatacaagaatatacaagtaacacccgtctgaattagaatctgttct 1380  
 Qy 1381 ttggaataatcaataatatttttgatgcgcgcgtgtgtgtgtccagatccatagctgt 1440  
 Db 1381 ttggaataatcaataatatttttgatgcgcgcgtgtgtgtgtccagatccatagctgt 1440  
 Qy 1441 gaagcttcggaagctgt 1500  
 Db 1441 gaagcttcggaagctgt 1500  
 Qy 1501 atggaattacgt 1560  
 Db 1501 atggaattacgt 1560  
 Qy 1561 gtggaacgaagtaacataagctcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1620  
 Db 1561 gtggaacgaagtaacataagctcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1620  
 Qy 1621 ctgaagaacacagctgt 1644  
 Db 1621 ctgaagaacacagctgt 1644

RESULT 4  
 AAX25718  
 ID AAX25718 standard; cDNA to mRNA; 1644 BP.  
 XX

AC AAX25718:  
 XX  
 DT 21-MAY-1999 (first entry)  
 XX  
 DE Firefly luciferase gene #4.  
 XX  
 KW Bioluminescent protein; catalytic efficiency; stability; firefly;  
 KW Luciferase; chimeric; Luciola cruciata; Luciola lateralis;  
 KW Photinus pyralis; primer; PCR; amplification; ss.  
 XX  
 OS Luciola lateralis.  
 OS Synthetic.  
 XX  
 PN W09902697-A1.  
 PD 21-JAN-1999.  
 XX  
 PF 30-JUN-1998; 98MO-JP02936.  
 XX  
 PR 08-JUL-1997; 97US-0051917.  
 XX  
 PA (KIKK ) KIKKOMAN CORP.  
 XX  
 PI Hirokawa K, Kajiyama N, Murakami S;  
 XX  
 DR WPI; 1999-120898/10.  
 DR P-PSDB; AAW93367.  
 XX  
 PT New bioluminescent protein with improved properties - has greater  
 PT catalytic efficiency and stability and is obtained by modification  
 of natural precursors  
 XX  
 PS Example 5; Page 35-36; 53pp; Japanese.  
 CC The invention relates to the generation of bioluminescent proteins with  
 CC improved catalytic efficiency and stability. The proteins are generated  
 CC by addition, deletion or substitution of amino acids from a precursor  
 CC protein e.g. firefly luciferases, or by constructing chimeric luciferase

CC proteins from luciferase genes from e.g. Luciola cruciata, L. lateralis  
 CC and Photinus pyralis. This sequence represents an example of a mutated  
 CC luciferase gene of the invention.  
 XX  
 SQ Sequence 1644 BP; 528 A; 260 C; 350 G; 506 T; 0 other.

Query Match 99.5%; Score 1636; DB 20; Length 1644;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 atggaacacatgagagacagatgaataatattgtatgtgtcctgaaccatttaccatt 60  
 Db 1 atggaacacatgagagacagatgaataatattgtatgtgtcctgaaccatttaccatt 60  
 Qy 61 gaagggagatcgtcgtgagacacatttgacgaatattatgattcgtatgcaaaacttga 120  
 Db 61 gaagggagatcgtcgtgagacacatttgacgaatattatgattcgtatgcaaaacttga 120  
 Qy 121 gcaattgctttacttaacgaactacccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180  
 Db 121 gcaattgctttacttaacgaactacccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180  
 Qy 181 aaatcaatgtctgttagagagagcgtttaagaattatgtgtgtgtgtgtgtgtgtgtgt 240  
 Db 181 aaatcaatgtctgttagagagagcgtttaagaattatgtgtgtgtgtgtgtgtgtgtgt 240  
 Qy 241 gcgttatcagtgaaacactgtgaagaattcttattcctgtattatgacgggttattata 300  
 Db 241 gcgttatcagtgaaacactgtgaagaattcttattcctgtattatgacgggttattata 300  
 Qy 301 ggtgctggt 360  
 Db 301 ggtgctggt 360  
 Qy 361 ggcattcttaagccaacattgtattttagttcttaaaaaaggattagataaagttaact 420  
 Db 361 ggcattcttaagccaacattgtattttagttcttaaaaaaggattagataaagttaact 420  
 Qy 421 gtacaaaaacggttaacgtctattaaacattgtattatgtgaagcgaagtgtgattat 480  
 Db 421 gtacaaaaacggttaacgtctattaaacattgtattatgtgaagcgaagtgtgattat 480  
 Qy 481 agaggtatacaatccatgtgacacatttataaaaaaacaccccaagggttccaaga 540  
 Db 481 agaggtatacaatccatgtgacacatttataaaaaaacaccccaagggttccaaga 540  
 Qy 541 tcaagttttaaactgtgaagttaacccgcaagaacaaagtgtcttataatgaactct 600  
 Db 541 tcaagttttaaactgtgaagttaacccgcaagaacaaagtgtcttataatgaactct 600  
 Qy 601 tcgggttaacccggtttgcgaagaagtgtgacacttaccatgagaataatgcctctaga 660  
 Db 601 tcgggttaacccggtttgcgaagaagtgtgacacttaccatgagaataatgcctctaga 660  
 Qy 661 ttcttcacgctagatgccaatattatgaaacaaagtttaccgagcagcgtctattta 720  
 Db 661 ttcttcacgctagatgccaatattatgaaacaaagtttaccgagcagcgtctattta 720  
 Qy 721 actgtagtaccattccatcatgt 780  
 Db 721 actgtagtaccattccatcatgt 780  
 Qy 781 ggtttcgatattgtatgtttaaagcaatttgacgaagagactttttaaaccactgcaa 840  
 Db 781 ggtttcgatattgtatgtttaaagcaatttgacgaagagactttttaaaccactgcaa 840  
 Qy 841 gattacaatgttcaagcgttattctgttacgcgacttgttgcgaatcttataatgaagt 900  
 Db 841 gattacaatgttcaagcgttattctgttacgcgacttgttgcgaatcttataatgaagt 900  
 Qy 901 gaattactcgataaataatgattatcaaatattagttgaatgtacatctgtgagagacact 960  
 Db 901 gaattactcgataaataatgattatcaaatattagttgaatgtacatctgtgagagacact 960

Db 901 gaattactcgaataatgatattatcaaatltagttgaattgacatctgcygagaccct 960  
QY 961 ttattctaaagaattggtgaagctgtgtctagacgttttaatttaccggtgtgtctca 1020  
XX |||||||  
Db 961 ttattctaaagaattggtgaagctgtgtctagacgttttaatttaccggtgtgtctca 1020  
QY 1021 ggcctatggtttacagaagaacacctgtgcaattatatacacacgggaagcgatgtataa 1080  
|||  
Db 1021 ggcctatggtttacagaagaacacctgtgcaattatatacacacgggaagcgatgtataa 1080  
QY 1081 ccaggtgtctctcgcaaaagtgtgtccattatcttaagaacaaagtatcgatcttgact 1140  
|||  
Db 1081 ccaggtgtctctcgcaaaagtgtgtccattatcttaagaacaaagtatcgatcttgact 1140  
QY 1141 aaaaaaacttggcccgacagacgttgagaagttgtgttaagggtcttaagtctatg 1200  
|||  
Db 1141 aaaaaaacttggcccgacagacgttgagaagttgtgttaagggtcttaagtctatg 1200  
QY 1201 aaaagttatgtagataatccagaagaacagaatacatagatgaagaagttgtgtg 1260  
|||  
Db 1201 aaaagttatgtagataatccagaagaacagaatacatagatgaagaagttgtgtg 1260  
QY 1261 cacaacagagatattggtgtatcagatgagaagaaacatttcttatacgtagatcgt 1320  
|||  
Db 1261 cacaacagagatattggtgtatcagatgagaagaaacatttcttatacgtagatcgt 1320  
QY 1321 aagctttaaatacaatacaagaagataatcaatcacctcgctgaattgaatctgtctt 1380  
|||  
Db 1321 aagctttaaatacaatacaagaagataatcaatcacctcgctgaattgaatctgtctt 1380  
QY 1381 ttgcaacatccaataattttttagatcgcgagctgtgtcgcttcacagatcctatagctgt 1440  
|||  
Db 1381 ttgcaacatccaataattttttagatcgcgagctgtgtcgcttcacagatcctatagctgt 1440  
QY 1441 gagcttcgggagctgtgtgttacttaagaagaagaatactatagctgtgtgtgtgtgtgt 1500  
|||  
Db 1441 gagcttcgggagctgtgtgttacttaagaagaagaatactatagctgtgtgtgtgtgtgt 1500  
QY 1501 atggattacgttgcagttcaagtttcaaatgcaaacgtttgcgtgtgtgtgtgtgtgtgt 1560  
|||  
Db 1501 atggattacgttgcagttcaagtttcaaatgcaaacgtttgcgtgtgtgtgtgtgtgtgt 1560  
QY 1561 gtggaacgaagtaacctaaagctcactgtgtaaatgacgtgaagaacgttaagaagaata 1620  
|||  
Db 1561 gtggaacgaagtaacctaaagctcactgtgtaaatgacgtgaagaacgttaagaagaata 1620  
QY 1621 ctgaagaacacagttgtctaaagt 1644  
|||  
Db 1621 ctgaagaacacagttgtctaaagt 1644

RESULT 5  
AA003257 standard; DNA; 1644 BP.  
XX  
AC AA003257;  
XX  
DT 22-JUL-1990 (first entry)  
XX  
DE Luciola lateralis recombinant luciferase gene.  
XX  
KW Luciferase; enzyme; ATP; plasmid pHLf7; firefly; ss.  
XX  
OS Luciola lateralis.  
XX  
FH Key Location/Qualifiers  
FT 1..1644  
FT /\*tag= a  
FT /product=Luciferase  
FT /EC\_number=EC-1.13.12.7  
XX  
EN EP353464-A.  
XX

PD 07-FEB-1990.  
XX  
PF 30-JUN-1989; 89EP-0111958.  
XX  
PR 22-DEC-1988; 88JP-0162402.  
PR 01-JUL-1988; 88JP-0162402.  
XX  
PA (KIKK ) KIKKOMAN CORP.  
XX  
XX Tatsumi H, Kajiyama N, Nakano E;  
PI WPI; 1990-038240/06.  
DR P-PSDB; AAR03731.  
XX  
PT New gene encoding Luciferase -  
PT derived from Luciola lateralis and expressed in and purified  
XX from Escherichia coli genus cells.  
XX  
PS Claim 3; page 24; 43pp; English.  
CC  
CC This enzyme is useful for determining ATP levels. It is  
XX contained in plasmid pHLf7.  
SQ Sequence 1644 BP; 529 A; 264 C; 348 G; 503 T; 0 other;

Query Match 99.3%; Score 1632.8; DB 11; Length 1644;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1637; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 1 atggaacacatggaagacatgaataatgtgtatgtgtcctgaaccattttaccctatt 60  
QY 61 gaagagagatctgtctgagacacattgtgcgaagatataatgatcagatatagcgaacttga 120  
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Db 61 gaagagagatctgtctgagacacattgtgcgaagatataatgatcagatatagcgaacttga 120  
QY 121 gaattgctttaaactaaacgacttaacggtgtgcgtatagatgacggaacttaagata 180  
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Db 121 gaattgctttaaactaaacgacttaacggtgtgcgtatagatgacggaacttaagata 180  
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Db 181 aaatcgtgtcctagagaagagctttaaagaattatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240  
QY 241 ggtatcagatggaagaactgtgaagaattccttattcctgtattagacgggtttattata 300  
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Db 241 ggtatcagatggaagaactgtgaagaattccttattcctgtattagacgggtttattata 300  
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Db 421 gtacaaaaaagcgttaactgtctatttaaacacattgttatattgtgacgcgaagtgtgatt 480  
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Db 481 agaggtatcaatccatgtaacacatttatataaaaaaacccccaagaagtttcaagaaga 540  
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|||  
Db 541 tcaagttttaaactgttagaagttaaacygaagaacaaagtgtgtcttataatgaaactct 600  
QY 601 tcgggttcaacccggttgcgcaaaaggtgtgtcaacttaccatcgaagaataatgttcaactaga 660  
|||  
Db 601 tcgggttcaacccggttgcgcaaaaggtgtgtcaacttaccatcgaagaataatgttcaactaga 660

QY 661 ttcttcacgctagagatcccaattatcgaaacccaagttccacgagcagcatttta 720  
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 QY 721 actgtaglacatccatcgcagtggttctgtatgttctactacttaagctactaactt 780  
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 Db 901 gaattactcgaataatgtatcttaacaaatttgaatttgcacatcgcgcagacact 960  
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 Db 1021 ggcatagttttaacagaacaacctctgcacattatcaacccgggaagcgatgataa 1080  
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 Db 1081 ccaggtgctctcgcgaagctgtgcatcttaataagcaaaagtatcgcattctgatact 1140  
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 Db 1141 aaaaaaactttggcccggaacagcgtggagaagtctgttgaagggctctctatgt 1200  
 QY 1201 aaaggtatgtagataatccagaagcaacagaagaatacatagatgaagaagtttggt 1260  
 Db 1201 aaaggtatgtagataatccagaagcaacagaagaatacatagatgaagaagtttggt 1260  
 QY 1261 cacaacagagatattgggtatcagatgaagaagaacattcttctatcgttgatcgtt 1320  
 Db 1261 cacaacagagatattgggtatcagatgaagaagaacattcttctatcgttgatcgtt 1320  
 QY 1321 aagttcttaatacaatacaagaagatatacagttaccacctgtgtaattagaatctgt 1380  
 Db 1321 aagttcttaatacaatacaagaagatatacagttaccacctgtgtaattagaatctgt 1380  
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 Db 1441 gagcttcgggagagctgtgtgttacttaagaagaagaatactatgactgtaaaaaagat 1500  
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 Db 1501 atggtatcgttctgtagtcaagttcaaatgcaaaagcttgcgtgtgtgtgtcgtttt 1560  
 QY 1561 gtgacggaagtacctaagaagctcactgttaaaattgacggttaagaacattagaaga 1620  
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 QY 1621 ctgaagaacacagttgtctaagatg 1644  
 Db 1621 ctgaagaacacagttgtctaagatg 1644

RESULT 6  
 AAT63269  
 ID AAT63269 standard; DNA; 1908 BP.

XX AC AAT63269;  
 XX DT 20-MAY-1997 (first entry)  
 XX DE Gene for firefly luciferase conjugated with 87 aa peptide at 3' end.  
 XX KW Fusion protein; firefly; luciola lateralis; luciferase; biotinylation;  
 XX KW wild type; E.coli; bioluminescence assay; quantification; ligand;  
 XX KW receptor; ds.  
 XX OS Synthetic.  
 XX FH Key  
 XX FH CDS 1..1641  
 XX FT /tag= a  
 XX FT /note= "encodes firefly portion of fusion protein"  
 XX FT CDS 1642..1647  
 XX FT /tag= b  
 XX FT /note= "sequence encoded by linker used to insert  
 FT sequence encoding biotin peptide to generate  
 FT fusion gene"  
 FT CDS 1648..1908  
 FT /tag= c  
 FT /note= "encodes biotinylated peptide portion of fusion  
 protein"  
 XX PN JP08308578-A.  
 XX PD 26-NOV-1996.  
 XX PF 24-APR-1995; 95JP-0098857.  
 XX PR 14-MAR-1995; 95JP-0054625.  
 XX PR 27-JUL-1994; 94JP-0193798.  
 XX PA (KIKR ) KIKKOMAN CORP.  
 XX DR WPI: 1997-059697/06.  
 XX DR P-PSDB; AAM12395.  
 XX PT Fusion protein comprising firefly luciferase and biotinylated  
 PT peptide - useful in a bio-luminescent analytical method for  
 PT quantifying ligands  
 XX PS Example 7; Page 11-12; 13pp; Japanese.  
 XX CC This is the nucleotide sequence encoding a novel fusion protein which  
 CC comprises the firefly (luciola lateralis) luciferase protein and an 87  
 CC amino acid biotinylated peptide designated the E.coli biotin carboxy  
 CC carrier protein (BCCP-87). The fusion gene was generated by firstly  
 CC amplifying the sequence encoding the E.coli (BCCP-87) from the E.coli  
 CC genome and inserting the resultant sequence into the 3' end of the  
 CC firefly luciferase gene in plasmid pHLf230. The biotin peptide sequence  
 CC replaces the C-terminal Met residue of the wild type luciferase sequence.  
 CC The plasmid was then introduced into E.coli JM101 for production of the  
 CC fusion protein. The novel protein can be used in bioluminescence assays  
 CC to quantify luciferase ligands which may modulate binding of luciferase  
 CC to its receptor.  
 XX XX  
 XX Sequence 1908 BP; 598 A; 329 C; 426 G; 555 T; 0 other;

Query Match 99.0%; Score 1628.2; DB 18; Length 1908;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1633; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
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 Db 1 atggaacaatcgtgagacgaatgaataatgtgtatcgtctgaacatttaccatt 60  
 QY 61 gaagaggatcgtcgtgagacgaatcgtgcaagatatgatcgtatgcaaaacttga 120  
 Db 61 gaagaggatcgtcgtgagacgaatcgtgcaagatatgatcgtatgcaaaacttga 120

Db 61 gaagaggatctgtcgtgagcacaaatgcgcaagtatatgatcagatatactgcaaaacttgga 120  
 QY 121 gaattgctttacttaacgcacttaacggtgtcogattactacgtacgcgaactacttagaa 180  
 Db 121 gaattgctttacttaacgcacttaacggtgtcogattactacgtacgcgaactacttagaa 180  
 QY 181 aaatcactgtctcgtcgaagaaggcttaagaattatggttctgtgtgtatgagtgaaagt 240  
 Db 181 aaatcactgtctcgtcgaagaaggcttaagaattatggttctgtgtgtatgagtgaaagt 240  
 QY 241 ggttatatgagtgaaagcgtgaagaattcttatctccgttatgtccggttatattata 300  
 Db 241 ggttatatgagtgaaagcgtgaagaattcttatctccgttatgtccggttatattata 300  
 QY 301 ggttcgtgtgtgtcccaactatgatattacactctacgtgaattgtgtccagttta 360  
 Db 301 ggttcgtgtgtgtcccaactatgatattacactctacgtgaattgtgtccagttta 360  
 QY 361 ggcactcctaaagccaaactatgtattagttcttaaaaaagattagataaagtataact 420  
 Db 361 ggcactcctaaagccaaactatgtattagttcttaaaaaagattagataaagtataact 420  
 QY 421 gtaaaaaaacgttaactgtctatataaacattgttatattgtgacgcgaagtgtattat 480  
 Db 421 gtaaaaaaacgttaactgtctatataaacattgttatattgtgacgcgaagtgtattat 480  
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 Db 481 agaggttalcactcaatgcacactttatataaaaaaacaccgccaaagtttccaagga 540  
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 Db 541 tcaagttttaaactgttagaagttaacgcgaagaacaagttgtctcttaataatgaactc 600  
 QY 601 tcgggttcaacccggtttgcccacaaaggtgtgcacacttaaccatgaagaatttcgcactaga 660  
 Db 601 tcgggttcaacccggtttgcccacaaaggtgtgcacacttaaccatgaagaatttcgcactaga 660  
 QY 661 ttcttcacgcgttagatcccaattatagtgaacccaagtttccacgcgcgcgtatatta 720  
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 Db 841 gattacaaatgttcaagcgttatctctgttacgcgactttgtgtcaattcttaataagaagt 900  
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 QY 1141 aaaaaaacttgggcccgaacagacgtgtgagaagttgtgttaaaaggtccctatgtatg 1200  
 Db 1141 aaaaaaacttgggcccgaacagacgtgtgagaagttgtgttaaaaggtccctatgtatg 1200

QY 1201 aaagtctatgatataatccagaagcaacagaagaatcatagatbaaaggttggtg 1260  
 Db 1201 aaagtctatgatataatccagaagcaacagaagaatcatagatbaaaggttggtg 1260  
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 Db 1621 ctgaagaacaacagttgctaaag 1641  
 RESULT 7  
 AAV32467  
 ID AAV32467 standard; DNA; 1920 BP.  
 XX  
 AC AAV32467;  
 XX  
 DT 10-SEP-1998 (first entry)  
 XX  
 DE Luciferase-lysostaphin fused gene.  
 XX  
 KW Luciferase-lysostaphin fused gene; chimeric; bioluminescence; ds.  
 XX  
 OS Chimeric - Staphylococcus simulans.  
 OS Chimeric - Luciola lateralis.  
 FH Key Location/Qualifiers  
 FT CDS 1..1920  
 FT /tag= a  
 FT /product= "Luciferase-lysostaphin fusion protein"  
 FT /note= "Nucleotides 1-1647 encode luciferase  
 protein while nucleotides 1648-1920 encode  
 lysostaphin; CDS does not contain stop codon"  
 PN JP10150991-A.  
 XX  
 PD 09-JUN-1998.  
 XX  
 PF 25-NOV-1996; 96JP-0328042.  
 XX  
 PR 25-NOV-1996; 96JP-0328042.  
 XX  
 PA (KIKK ) KIKKOMAN CORP.  
 XX  
 DR WPI; 1998-379994/33.  
 DR P-PSDB; AAW48856.  
 XX  
 PT New luciferase-lysostaphin fused protein - useful for  
 XX bioluminescence analysis

PS Disclosure; Pages 6-7; 10pp; Japanese.

XX The invention claims for a luciferase-lystostaphin fused gene which encodes a fused protein in which a peptide part consisting of luciferase, from *Luciola lateralis*, is connected to a peptide part consisting of lystostaphin from *Staphylococcus simulans*. The method described by the invention can be used to prepare a luciferase-lystostaphin fused protein efficiently. The fused protein is useful for bioluminescence analysis.

CC  
XX Sequence 1920 BP; 627 A; 310 C; 407 G; 576 T; 0 other;

Query Match 99.0%; Score 1628.2; DB 19; Length 1920;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1633; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 1621 ctgaagaacacaaagtgtctaag 1641
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RESULT 8  
AAT33850  
ID AAT33850 standard; DNM; 2019 BP.  
XX  
AC AAT33850;  
XX  
DT 12-NOV-1996 (first entry)  
XX  
DE DNA encoding streptavidin/luciferase fusion protein.  
XX  
XX Streptavidin; luciferase; fusion protein;  
XX Streptomyces avidinii; *Luciola lateralis*; firefly;  
XX recombinant production; industry; ds.  
OS Synthetic.  
XX

Key Location/Qualifiers  
 CDS 1..2019  
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JP07289264-A.  
 07-NOV-1995.  
 27-APR-1994; 94JP-0090275.  
 27-APR-1994; 94JP-0090275.  
 27-APR-1994; 94JP-0090275.  
 (KIKK ) KIRKMAN CORP.  
 MPI: 1996-015269/02.  
 P-PSDB: AAM04208.

New mutant streptavidin (SA) gene - fused to a firefly luciferase gene, for the recombinant prepn. of a SA-FL fused protein

Example 1; Pages 5-6; 12pp; Japanese.

The present sequence encodes a streptavidin/luciferase fusion protein, comprising the Streptomyces avidinii streptavidin gene and the Luciola lateralis (firefly) luciferase gene. The fusion protein can be prepd. by inserting the recombinant DNA encoding it into a Escherichia species microbe, culturing the transformed microbe in a medium and collecting the fusion protein from the culture. The fusion protein can be used in industry.

Sequence 2019 BP; 590 A; 412 C; 467 G; 550 T; 0 other;

Query Match 98.5%; Score 1620; DB 17; Length 2019;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 1626; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 9 catgagagacgtgaaatattgtatgttcttgaaacatttaccatttgaagagg 68  
 DB 384 cctcgagagacgtgaaatattgtatgttcttgaaacatttaccatttgaagagg 443  
 QY 69 atctctgtgagacgaattgacgaatataatgatacgaataaacttgagcaattgc 128  
 DB 444 atctctgtgagacgaattgacgaatataatgatacgaataaacttgagcaattgc 503  
 QY 129 ttcttaacgacactaccggtgtgcgattatagctgacgacgaatacttgaagaacatcg 188  
 DB 504 ttcttaacgacactaccggtgtgcgattatagctgacgacgaatacttgaagaacatcg 563  
 QY 189 ctgtctagagagagccttaagaatattgttggttgttgaatgagaaatgctgtatg 248  
 DB 564 ctgtctagagagagccttaagaatattgttggttgttgaatgagaaatgctgtatg 623  
 QY 249 cagtgaataacgttgaagaattcttattcctgtatattagccggttattatagtggtcgg 308  
 DB 624 cagtgaataacgttgaagaattcttattcctgtatattagccggttattatagtggtcgg 683  
 QY 309 tctgtgtccaaatgaatgatttacccttaccgtgaattggttgcaggtttagcatttc 368  
 DB 684 tctgtgtccaaatgaatgatttacccttaccgtgaattggttgcaggtttagcatttc 743  
 QY 369 taagcacaacttgaatttcttcttaaaagagattagataaagttatattactgtaca 428  
 DB 744 taagcacaacttgaatttcttcttaaaagagattagataaagttatattactgtaca 803  
 QY 429 aacggttaactgtattataaaccattgttatattgacagcaagtggtattatagaggtta 488  
 DB 804 aacggttaactgtattataaaccattgttatattgacagcaagtggtattatagaggtta 863  
 QY 489 tcaatccatgtgcaacttattataaataaactccacaaagtttccaagagttcaagtt 548  
 DB 864 tcaatccatgtgcaacttattataaataaactccacaaagtttccaagagttcaagtt 923

QY 549 taaactgtagagattaccgcaagaacgaattgtctcttataatgaacttcgggttc 608  
 DB 924 taaactgtagagattaccgcaagaacgaattgtctcttataatgaacttcgggttc 983  
 QY 609 aacggttgcacaaagtgctgacacttaccatgaanaatctgcatagattttctca 668  
 DB 984 aacggttgcacaaagtgctgacacttaccatgaanaatctgcatagattttctca 1043  
 QY 669 cgtctagagatccaaattttagaagaacgaatttccacagcagcggttattactgt 728  
 DB 1044 cgtctagagatccaaattttagaagaacgaatttccacagcagcggttattactgt 1103  
 QY 729 accattccatcagtggttctgatacttactacttacttacttacttacttacttact 788  
 DB 1104 accattccatcagtggttctgatacttactacttacttacttacttacttacttact 1163  
 QY 789 tattgtcatgttaacgaataattgacgaagagactttttaaataacatgcaagattaca 848  
 DB 1164 tattgtcatgttaacgaataattgacgaagagactttttaaataacatgcaagattaca 1223  
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 QY 1029 ttttaacagaacacacttgcacatttataccacccggaagcgatgaacccaagttgc 1088  
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 QY 1089 ttctgtgcaagttgtgcatattttaaagcaaaagttatcgatctgtatatactaa 1148  
 DB 1464 ttctgtgcaagttgtgcatattttaaagcaaaagttatcgatctgtatatactaa 1523  
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 DB 1524 ttgtggcccggaacagacgtgtggaagattgtgttaagagttctatgtatgaaggtta 1583  
 QY 1209 tgtagaataatccagaagcaacagaagaatccatagaatgaagaagttgtgtcacacagg 1268  
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 DB 1704 aatcaataatcaagaatatacaagttaccactgtgtaattagaatctgttctttgca 1763  
 QY 1389 tccaataatttttgaatgcccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1448  
 DB 1764 tccaataatttttgaatgcccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1823  
 QY 1449 gggagcgt 1508  
 DB 1824 gggagcgt 1883  
 QY 1509 cgttgcgtgcaagtttcaaatgcaaaaagtttgggtgtgtgtgtgtgtgtgtgtgt 1568  
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 QY 1569 agttacaaagttcctcaactgtcaaaattgacggttaaaagaaattagaataactga 1628  
 DB 1944 agttacaaagttcctcaactgtcaaaattgacggttaaaagaaattagaataactga 2003  
 QY 1629 accagttgctaagatg 1644

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Db      2004      accagttgctaagatg      2019
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RESULT	9
AAT33851	
ID	AAT33851 standard; DNA; 2055 BP

DT 12-NOV-1996 (first entry)

DE DNA encoding mutant streptavidin/luciferase fusion protein.

KW Mutant; streptavidin; luciferase; fusion protein;  
KW Streptomyces avidinii; *Luciola lateralis*; firefly;  
KW recombinant production; industry; ds.

Synthetic.

FH	Key	Location/Qualifiers
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100	100	100

/\*tag = a

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FT      /note= "STOP codon absent"
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PN JP07289264-A.

PD 07-NOV-1995.

PF 27-APR-1994; 94JP-0090275.

PR 27-APR-1994; 94JP-0090275.

PA (KIKK ) KIKKOMAN CORP.

DR WPI; 1996-015269/02.

DR P-PSDB; AAW04208.

PT New mutant streptavidin (SA) gene - fused to a firefly luciferase

PT gene, for the recombinant prepn. of a SA-FL fused protein

PS Claim 1; pages 7-8; 12pp; Japanese.  
XX

CC The present sequence encodes a mutant streptavidin/luciferase  
CC fusion protein comprising a mutant streptomycin avidin!

fusion protein, comprising a mutant streptomyces avidin-luciferase fusion gene and the *Luciola lateralis* (firefly) luciferase gene.

gene. The fusion protein can be prepd. by inserting the

recombinant DNA encoding it into a *Escherichia* species microbe,

CC culturing the transformed microbe in a medium and collecting the

CC fusion protein from the culture. The fusion protein can be used

CC in industry.

50 Sequence 2055 BP; 603 A; 418 C; 474 G; 560 T; 0 other;

Country	Year	Value
China	1990	1.00
China	1991	1.00
China	1992	1.00
China	1993	1.00
China	1994	1.00
China	1995	1.00
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China		

Query Match	98.58;	Score 1620;	DB 17;	Length 2055;
Best Local Similarity	99.48;	Prod NO. 0;		

Best Local Similarity 99.4%; Pred. No. 0;  
Matches 1626; Conservative 0; Mismatches

MACHINES 1020, CONSERVATIVE 0, MISMA LINES 10, ANGLES 0, GAPS 0,

QY 9 cggaggaagacatataaaatatttgatgatggtccgaaccccttaacccattgaagagg 68  
DB 420 cctcgagaagacgtgaaaatattgtgatggtcccggaacatttaacctattgaagagg 479  
QY 69 atctgctggaagacacattgctgcaagtatatagtatgcatalgtcaaaacttggaagattgc 128  
DB 480 atctgctggaagacacattgctgcaagtatatagtatgcatalgtcaaaacttggaagattgc 539  
QY 129 ttcttctaagcacttaccggtgtcgatatacgttaacgtaacgaatcttagaataaatatg 188  
DB 540 ttcttctaagcacttaccggtgtcgatatacgttaacgtaacgcaaatcttagaataaatatg 599  
QY 189 ctgtctagaagagccttcaagaattatggttttggtttgtatggaagattgcgttatg 248

Db	600	ctgctcctagsgagagcctttaagaatactggtttggttgctgtagtgaaagaatttcggtta	559
Qy	249	caatgtaaacactgtgaagaattctcttacttcgcgttatctagaacggttatthataagtgctcg	308
Db	660	cagtgaaacactgtgaagaagtcttcttacttccttgctatctagaacggtttattatagtgctcg	719
Qy	309	tgtgctccaaactaataatgaattcaactctacgtgaattggtttcaacggttaggcattcc	368
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Qy	369	taagccacaactgttatttgcctcttaaaaaagattagaataaagtattaaactgtaca	428
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Qy	429	aacgtaactgtcttaataaacactgtttatctatctgacgcgaagtgttaataaggtta	488
Db	840	aacgtaactgtcttaataaacactgtttatctatctgacgcgaagtgttaataaggtta	899
Qy	489	tcaatccatgtgacaactttataaaaaaacaccaccacaaggttccaaggtccaagttc	548
Db	900	tcaatccatgtgacaactttataaaaaaacaccaccacaaggttccaaggtccaagttc	959
Qy	549	taaaactgtgaagtttaacgcgcaagaacaaagtgtgccttataatgaactcttcgggttc	608
Db	960	taaaactgtgaagtttaacgcgcaagaacaaagtgtgccttataatgaactcttcgggttc	1019
Qy	609	aaccggtttgcgaagaagtgtgtcaacttactcaatgaaatcatcgtcacatgaattcttca	668
Db	1020	aaccggtttgcgaagaagtgtgtcaacttactcaatgaaatcatcgtcacagcgttttctca	1079
Qy	669	cgcttagagatcccaatttataatgaaaccaagtcttaccacgcgcgctatttaactgtagt	728
Db	1080	cgcttagagatcccaatttataatgaaaccaagtcttaccacgcgcgctatttaactgtagt	1139
Qy	729	accattccatcaatggtttgtgtatggttactactttaggtacttcaactgtggtttctg	788
Db	1140	accattccatcaatggtttgtgtatggttactactttaggtacttcaactgtggtttctg	1199
Qy	789	tattgtcaatgttaacgcgaattctgacgaagaagactttttaaaacacgcgcaagtttcaa	848
Db	1200	tattgtcaatgttaacgcgaattctgacgaagaagactttttaaaacacgcgcaagtttcaa	1259
Qy	849	atgttcaacgcgttacttctgttaccgcgacttgttgtgcaattcttcaataagatgaattact	908
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Qy	909	cgataaataatgaattatccaatttgaattgtgaattgcatcttgcgcgagacactttatctaa	968
Db	1320	cgataaataatgaattatccaatttgaattgtgaattgcatcttgcgcgagacactttatctaa	1379
Qy	969	agaataatgtgaacgtgttgcctagacgcttttaataccgcggtgtctgcaagctatg	1028
Db	1380	agaataatgtgaacgtgttgcctagacgcttttaataccgcggtgtctgcaagctatg	1439
Qy	1029	ttttaaacgaagaacacccctctgcaattatatacaccgcgaagcgatgataaacgagtc	1088
Db	1440	ttttaaacgaagaacacccctctgcaattatatacaccgcgaagcgatgataaacgagtc	1499
Qy	1089	tctctgcaagaatgttgcctatattttaagcgaagaatgtaatcgatcttgatactataaaaaac	1148
Db	1500	tctctgcaagaatgttgcctatattttaagcgaagaatgtaatcgatcttgatactataaaaaac	1559
Qy	1149	tttggtcccggaacgacgtgagagaagtgtgtgtaaaagggtccatgactatgaagaagctta	1208
Db	1560	tttggtcccggaacgacgtgagagaagtgtgtgtaaaagggtccatgactatgaagaagctta	1619
Qy	1209	tgtatagataatccagaagaacaaagagaatacatagataagaagaagtttggtgtgcacacag	1268
Db	1620	tgtatagataatccagaagaacaaagagaatacatagataagaagaagtttggtgtgcacacag	1679
Qy	1269	agatatgtggtattacgataatgaagaanaaacattcttatacgttgatcgtttgaagctctt	1328
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 QY 1569 agtacttaaaaggtccactgcgtgtaaaattgacggttaagaacattagaagaactgaaga 1628  
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 Db 1980 agtacttaaaaggtccactgcgtgtaaaattgacggttaagaacattagaagaactgaaga 2039  
 QY 1629 accagttgctaagatg 1644  
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 Db 2040 accagttgctaagatg 2055

## RESULT 10

AAT63268  
 ID AAT63268 standard; DNA; 1704 BP.

AC AAT63268;

DT 20-MAY-1997 (first entry)

Firefly Luciferase conjugated with 23 aa peptide at 5' end.

FW Fusion protein; firefly; Luciola lateralis; Luciferase; biotinylation;  
 KW wild type; E.coli; bioluminescence assay; quantification; ligand;  
 KM receptor; ds.

OS Synthetic.

XX Key Location/Qualifiers

FT 1..75

FT CDS

/\*tag= a  
 /note= "encodes biotinylated peptide"

FT 76..1704

FT /\*tag= b

FT /note= "encodes firefly luciferase residues 4-54"

XX JP08308578-A.

PN 26-NOV-1996.

XX 24-APR-1995; 95JP-0098857.

PF 14-MAR-1995; 95JP-0054625.

PR 27-JUL-1994; 94JP-0193798.

XX (KIKK ) KIKKOMAN CORP.

PA WPI: 1997-059697/06.

XX P-PSDB; AAW12394.

DR Fusion protein comprising firefly luciferase and biotinylated

XX peptide - useful in a bio-luminescent analytical method for

PT quantifying ligands

XX Example 1; Page 9-10; 13pp; Japanese.

PS This is the nucleotide sequence encoding a novel fusion protein which

XX comprises the firefly (Luciola lateralis) luciferase protein and a

CC 23 amino acid biotinylated peptide designated biotin peptide #84.

CC The gene was generated by firstly annealing the sequence encoding  
 CC peptide #84 (AAT63270) and its complementary sequence, then inserting the  
 CC resultant double stranded sequence into the 5' end of the luciferase gene  
 CC in plasmid pHF108. The biotin peptide sequence replaces the first 4  
 CC amino acids of the wild type luciferase sequence. The plasmid was then  
 CC introduced into E.coli JM101 for production of the fusion protein. The  
 CC novel protein can be used in bioluminescence assays to quantify  
 CC luciferase ligands which may modulate binding of luciferase to its  
 CC receptor.  
 CC  
 SQ Sequence 1704 BP; 541 A; 275 C; 361 G; 527 T; 0 other;

Query Match 98.5%; Score 1619.6; DB 18; Length 1704;

Best local similarity 99.4%; Pred. No. 0;

Matches 1625; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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 QY 131 ttactaacgcaacttaacggtgtgcgatatacgtacgcgcgaactatagaaatcatgct 190  
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 QY 251 gttgaacgtgtgaagaattcttattccctgtatagccggttattataggtgtcggtg 310  
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 QY 311 tggctccaactaatgattatgactctacgtgaattgtgtacagtttaggcactctca 370  
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 QY 371 agccaacattgtatttagttcttaaaaaagattagataaagttataactgtacaaaaa 430  
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 QY 431 cggtaacctatlaaaaccattgttatatgtgacgcgaagttgattatagagttacc 490  
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 QY 491 aatcatgacacacttatttaaaaaaacatccacaaggtttcaaaagatcaatttta 550  
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 Db 551 aatcatgacacacttatttaaaaaaacatccacaaggtttcaaaagatcaatttta 610  
 QY 551 aaactgtagaatttaacgcgaagaacaggtgtccttataatgtaactcttggttcaa 610  
 |||||||  
 Db 611 aaactgtagaatttaacgcgaagaacaggtgtccttataatgtaactcttggttcaa 670  
 QY 611 ccggtttgcgaagaaggtgtgcgaactactcatgaataattgtgtcgcggtttttctcacg 670  
 |||||||  
 Db 671 ccggtttgcgaagaaggtgtgcgaactactcatgaataattgtgtcgcggtttttctcacg 730  
 QY 671 cttagatccaatttatggaacccaagtttcaacgcgcgcggtatatttaactgtatgac 730  
 |||||||  
 Db 731 cttagatccaatttatggaacccaagtttcaacgcgcgcggtatatttaactgtatgac 790  
 QY 731 cattccatcatggtttgtgtatgttactactttaggcattactactgtgttttgta 790  
 |||||||  
 Db 791 cattccatcatggtttgtgtatgttactactttaggcattactactgtgttttgta 850  
 QY 791 ttgtcatgttaacgaatttgacgaagagactttttaaaacactgcgaagttacaat 850  
 |||||||  
 Db 851 ttgtcatgttaacgaatttgacgaagagactttttaaaacactgcgaagttacaat 910



QY 851 gtccaagcgtatcttctgtacccgacttgttgcacattcttaataagatgaactacg 910  
 |||||||  
 DB 911 gtccaagcgtatcttctgtacccgacttgttgcacattcttaataagatgaactacg 970  
 |||||||  
 QY 911 ataataatgatattcaaatattagttgaatctgcctgcgagacacttcttaag 970  
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 DB 971 ataataatgatattcaaatattagttgaatctgcctgcgagacacttcttaag 1030  
 |||||||  
 QY 971 aaatttggaagctgttgcagacgttttaattaccgggtgttcgaaggtatggt 1030  
 |||||||  
 DB 1031 aaatttggaagctgttgcagacgttttaattaccgggtgttcgaaggtatggt 1090  
 |||||||  
 QY 1031 taacagaataaacactctgcacattatcacaccgggaagcgaatgaataacggctgt 1090  
 |||||||  
 DB 1091 taacagaataaacactctgcacattatcacaccgggaagcgaatgaataacggctgt 1150  
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 QY 1091 ctggcaaatgttgcacattatttaagcaaatgtatcgacttgcataactaaact 1150  
 |||||||  
 DB 1151 ctggcaaatgttgcacattatttaagcaaatgtatcgacttgcataactaaact 1210  
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 QY 1151 tggggccgacacagcgtgggaagttgttgaaggttcctatgcttgaagaaggtatg 1210  
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 DB 1211 tggggccgacacagcgtgggaagttgttgaaggttcctatgcttgaagaaggtatg 1270  
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 QY 1211 tagataatccagaagcacacagaagaatcatagatgaagaaggttggttgcacacggag 1270  
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 DB 1271 tagataatccagaagcacacagaagaatcatagatgaagaaggttggttgcacacggag 1330  
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 QY 1271 atattgggtatccagatgaagaataacattcttaccgttgcgttgaagctttaa 1330  
 |||||||  
 DB 1331 atattgggtatccagatgaagaataacattcttaccgttgcgttgaagctttaa 1390  
 |||||||  
 QY 1331 tcaaatcaagaagatatacaagttaccactgtcgaattagaatgttcttcttcaacatc 1390  
 |||||||  
 DB 1391 tcaaatcaagaagatatacaagttaccactgtcgaattagaatgttcttcttcaacatc 1450  
 |||||||  
 QY 1391 caaatatttttgatgcgcggtgttgcgttccagatccctatagctggtgagcttcgg 1450  
 |||||||  
 DB 1451 caaatatttttgatgcgcggtgttgcgttccagatccctatagctggtgagcttcgg 1510  
 |||||||  
 QY 1451 gagctgttctgtacttaagaagaataatctatgactgtaagaagaagtaagtatgacg 1510  
 |||||||  
 DB 1511 gagctgttctgtacttaagaagaataatctatgactgtaagaagaagtaagtatgacg 1570  
 |||||||  
 QY 1511 ttgtctagtcgaagttcaaatgcaaaacgttgcgttgcgttgcgttgcgttgcgttgcgt 1570  
 |||||||  
 DB 1571 ttgtctagtcgaagttcaaatgcaaaacgttgcgttgcgttgcgttgcgttgcgttgcgt 1630  
 |||||||  
 QY 1571 taccataagttctcactgcttaaatgtacgtaagaagaatctagaagaatactgaagaac 1630  
 |||||||  
 DB 1631 taccataagttctcactgcttaaatgtacgtaagaagaatctagaagaatactgaagaac 1690  
 |||||||  
 QY 1631 caagtctgaagatg 1644  
 |||||||  
 DB 1691 caagtctgaagatg 1704  
 |||||||

## RESULT 11

AAV233595 standard; cDNA to mRNA; 1704 BP.

AC AAV233595;

DT 16-JUL-1998 (first entry)

DE Antibody-Firefly Luciferase fusion protein gene.

KM Firefly Luciferase; antibody-Luciferase fusion protein; ds.

OS Luciola cruciata.

XX Key Location/Qualifiers

FH CDS 1..1704

FT /\*tag= a  
 FR /note= "no stop codon given"  
 PN JP09187281-A.  
 XX 22-JUL-1997.  
 PD 09-JAN-1996; 96JP-0001812.  
 XX 09-JAN-1996; 96JP-0001812.  
 PR 09-JAN-1996; 96JP-0001812.  
 XX (KIKK ) KIKKOMAN CORP.  
 PA WPI; 1998-275089/25.  
 DR P-PSDB; AAM53883.  
 PT Antibody-firefly Luciferase fused protein - and related products  
 PT i.e. firefly Luciferase fused gene, recombinant DNA and its  
 PS preparation  
 PS Disclosure: Page 10-11; 17pp; Japanese.  
 CC This sequence encodes a fusion protein of the invention. The protein is  
 CC a antibody-firefly Luciferase fusion protein, in which an antibody part  
 CC consisting of a peptide having antibody activity is combined with an  
 CC enzyme part consisting of firefly Luciferase.  
 XX  
 SO Sequence 1704 BP; 541 A; 275 C; 361 G; 527 T; 0 other;

Query Match 98.5%; Score 1619.6; DB 19; Length 1704;  
 Best Local Similarity 99.4%; Pred. No. 0;  
 Matches 1625; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 11 tggagaagcagatgaataattgtgtatgtgtcccgacacatttaccctattgaagagat 70  
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 DB 71 tggagaagcagatgaataattgtgtatgtgtcccgacacatttaccctattgaagagat 130  
 |||||||  
 QY 71 ctgctgagacacatgtgcgaagtatgtatgcgatalgcgaatacttgaagaaggtat 130  
 |||||||  
 DB 131 ctgctgagacacatgtgcgaagtatgtatgcgatalgcgaatacttgaagaaggtat 190  
 |||||||  
 QY 131 ttactaacgacttaccggtgttcgattatgaatgcgacgaatacttgaagaaggtat 190  
 |||||||  
 DB 191 ttactaacgacttaccggtgttcgattatgaatgcgacgaatacttgaagaaggtat 250  
 |||||||  
 QY 191 gttcagaagaagcgttgaagaatattggttgcgttgcgttgcgttgcgttgcgttgcgt 250  
 |||||||  
 DB 251 gttcagaagaagcgttgaagaatattggttgcgttgcgttgcgttgcgttgcgttgcgt 310  
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 QY 251 gttcagaagaagcgttgaagaatattggttgcgttgcgttgcgttgcgttgcgttgcgt 370  
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 DB 311 gttcagaagaagcgttgaagaatattggttgcgttgcgttgcgttgcgttgcgttgcgt 370  
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 QY 311 tggctccaactaatgagatttacaactctacgtgaattgttgcagatttaggcactcta 370  
 |||||||  
 DB 371 tggctccaactaatgagatttacaactctacgtgaattgttgcagatttaggcactcta 430  
 |||||||  
 QY 371 agccaacaattgtatttgcgttcaaaaagattatgaagaattatgaagaattatgaaga 430  
 |||||||  
 DB 431 agccaacaattgtatttgcgttcaaaaagattatgaagaattatgaagaattatgaaga 490  
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 QY 431 cgttaactgtctatgaacacattgtattatgtgaagcgaagttgattatgaagaattatc 490  
 |||||||  
 DB 491 cgttaactgtctatgaacacattgtattatgtgaagcgaagttgattatgaagaattatc 550  
 |||||||  
 QY 491 aatcagtgacacatttataaaaacaccccaagaagttcaagaagttatca 550  
 |||||||  
 DB 551 aatcagtgacacatttataaaaacaccccaagaagttcaagaagttatca 610  
 |||||||  
 QY 551 aaactgtagaagtttaacgcgaagaagaagttgcttctataatgaagcttgcgttcaa 610  
 |||||||  
 DB 611 aaactgtagaagtttaacgcgaagaagaagttgcttctataatgaagcttgcgttcaa 670  
 |||||||

QY	611	ccggttgcgcaaaaggtgtgtaacttactcaatgaataatcgtcactagattttctcaag	670
Db	671	ccggctctgcgcaaaaggtgtgtaacttactcaatgaataatctgtgttcacag	730
QY	671	ctagaatcccaattatagaaccaagttccacagacagcgctattttaaactgtatgc	730
Db	731	ctagaatcccaattatagaaccaagttccacagacagcgctattttaaactgtatgc	790
QY	731	cattccatcaggttttggtatgttttactacttaaggctactcaactgtgtgttcgtat	790
Db	791	cattccatcaggttttggtatgttttactacttaaggctactcaactgtgtgttcgtat	850
QY	791	ttgtcatgttacaagaatttgcagaagagctttttaaaaacacgtcaagatataaact	850
Db	851	ttgtcatgttacaagaatttgcagaagagctttttaaaaacacgtcaagatataaact	910
QY	851	gttcaagcgttattctctgttaccgacttgttgcgaatttctaataagatgaattactcg	910
Db	911	gttcaagcgttattctctgttaccgacttgttgcgaatttctaataagatgaattactcg	970
QY	911	ataaatatgatttttcaaatatgaattgaattgaattcgtcgtcgagacacttattctaaag	970
Db	971	ataaatatgatttttcaaatatgaattgaattgaattgaattcgtcgtcgagacacttattctaaag	1030
QY	971	aaatgtgtgaagcggtgtgttgcataagcgttttattacccgggtgttcgtcaagcgtatggt	1030
Db	1031	aaatgtgtgaagcggtgtgttgcataagcgttttattacccgggtgttcgtcaagcgtatggt	1090
QY	1031	taacgcgaaacaacctctgcataattatctacacccggagaagcgatgataaaccagtgctt	1090
Db	1091	taacgcgaaacaacctctgcataattatctacacccggagaagcgatgataaaccagtgctt	1150
QY	1091	ctgcgaagaagtgtgcattatttaagaacaaagttatcgatcttgcacttaaaaaactt	1150
Db	1151	ctgcgaagaagtgtgcattatttaagaacaaagttatcgatcttgcacttaaaaaactt	1210
QY	1151	ttggcccggaacagacgttgcgaagaagttgttgaaggtctcatgctatgctatgaagaagttatg	1210
Db	1211	ttggcccggaacagacgttgcgaagaagttgttgaaggtctcatgctatgctatgaagaagttatg	1270
QY	1211	tagaataatccgaagcagaacagagaatactatagaagaaggttgtgtgcacacagag	1270
Db	1271	tagaataatccgaagcagaacagagaatactatagaagaaggttgtgtgcacacagag	1330
QY	1271	atatgtggttatacgaatgaagaanaaaacattctcttactcgtgtgacgttgcgaactttaa	1330
Db	1331	atatgtggttatacgaatgaagaanaaaacattctcttactcgtgtgacgttgcgaactttaa	1390
QY	1331	tcaaatatacaagatatacaagttaccacccgtcgtgaattagaatcgttctctttgcacacatc	1390
Db	1391	tcaaatatacaagatatacaagttaccacccgtcgtgaattagaatcgttctctttgcacacatc	1450
QY	1391	caaatatttttgaatgcgcggcgttgcgtgcgtcttccgaatccctaaagtcttgcgttcgcgg	1450
Db	1451	caaatatttttgaatgcgcggcgttgcgtgcgtcttccgaatccctaaagtcttgcgttcgcgg	1510
QY	1451	gagcgtgtgttgtactctgaanaaagaanaactctatgactgaanaaagaanaatgattactag	1510
Db	1511	gagcgtgtgttgtactctgaanaaagaanaactctatgactgaanaaagaanaatgattactag	1570
QY	1511	ttgtcgtatgcaagtttcaaatgcaaaacggtttggtgtgtgtgttcogtttttgcgcgag	1570
Db	1571	ttgtcgtatgcaagtttcaaatgcaaaacggtttggtgtgtgtgtgttcogtttttgcgcgag	1630
QY	1571	taccataaaggtctcactcgtgataaattgacggtataaagaattagagaataactcgaagaac	1630
Db	1631	taccataaaggtctcactcgtgataaattgacggtataaagaattagagaataactcgaagaac	1690
QY	1631	caagtgtcgaagatg 1644	
Db	1691	caagtgtcgaagatg 1704	

RESULT	12
AAV23580	
ID	AAV23580 standard; cDNA to mRNA; 2364 BP.
XX	
AC	AAV23580;
XX	
DT	16-JUL-1998 (first entry)
XX	
DE	Antibody-firefly luciferase fusion protein gene.
XX	
KW	Firefly luciferase; antibody-luciferase fusion protein; ds.
XX	
OS	Luciola cruciata.
XX	
FH	Key
FT	Location/Qualifiers
FT	CDS
FT	1..2364
FT	*tag= a
FT	/transl_except= (pos: 670..672, aa: Glu)
FT	/transl_except= (pos: 739..741, aa: Trp)
FT	/transl_except= (pos: 1369..1371, aa: Ala)
FT	/note= "no stop codon given"
FT	
XX	
PN	JP09187281-A.
XX	
PD	22-JUL-1997.
XX	
PF	09-JAN-1996; 96JP-0001812.
XX	
PR	09-JAN-1996; 96JP-0001812.
XX	
PA	(KIKK ) KIRKOMAN CORP.
XX	
DR	WPI; 1998-275089/25.
XX	
DR	P-PSDB; AAM53882.
XX	
PT	Antibody-firefly luciferase fused protein - and related products
PT	i.e. firefly luciferase fused gene, recombinant DNA and its
PT	preparation
XX	
XX	Disclosure; Page 13; 17pp; Japanese.
XX	
CC	This sequence encodes the fusion protein of the invention. The protein is
CC	a antibody-firefly luciferase fusion protein, in which an antibody part
CC	consisting of a peptide having antibody activity is combined with an
CC	enzyme part consisting of firefly luciferase.
XX	
SO	Sequence 2364 BP; 697 A; 444 C; 559 G; 664 T; 0 other;
<hr/>	
Query Match	98.4%; Score 1618.4; DB 19; Length 2364;
Best Local Similarity	99.3%; Pred. No. 0;
Matches 1625; Conservative	0; Mismatches 11; Indels 0; Gaps 0.
<hr/>	
OY	9 catggagaagcgtgaaaatatgtctatgttcctgaaccatttaccctatgaagagg 68
Db	1   ttttgaaacgcgtgtaaacatattgttatgttcctgaaccatttaccctatgaagagg 788
OY	69 atctgcctggagcaccaattgcgaagtatatgatctgatgacaacacttgagcaattgc 128
Db	789 attctgcctggagcaccaattgcgaagtatatgatctgatgacaacacttgagcaattgc 848
OY	129 tttaactaacgcaacttacccggtgtcgattatccgtaagccggaataacttagaaaaatcatg 188
Db	849 tttaactaacgcaacttacccggtgtcgattatccgtaagccggaataacttagaaaaatcatg 908
OY	189 ctgtctagagagagcgtttaaagaatcatcgtttgttgttgaatggagaagtgcgtatg 248
Db	909 ctgtctagagagagcgtttaaagaatcatcgtttgttgttgaatggagaagtgcgtatg 968
OY	249 caatgaaaaactgtgaagaattcttatccctgtatcattagccggcttatattataggtgtcgg 308
Db	969 caatgaaaaactgtgaagaattcttatccctgtatcattagccggcttatattataggtgtcgg 1028

QY 309 tglgtcccaactaagtattacactacgtgaattgtgtccacagtttagcatctc 368  
 Db 1029 tglgtcccaactaagtattacactacgtgaattgtgtccacagtttagcatctc 1088  
 QY 369 taagccaacattgtattagttcttaaaaaaggattagataaagttataactgtcaaaa 428  
 Db 1089 taagccaacattgtattagttcttaaaaaaggattagataaagttataactgtcaaaa 1148  
 QY 429 aacggttaactgtattataaacattgttattatggaccgcaagtgattataagtgta 488  
 Db 1149 aacggttaactgtattataaacattgttattatggaccgcaagtgattataagtgta 1208  
 QY 489 tcaatccaggaacaacttattataaaaaaacctccacaaggttccaagaagtcagtt 548  
 Db 1209 tcaatccaggaacaacttattataaaaaaacctccacaaggttccaagaagtcagtt 1268  
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 Db 1269 taaactgtagaagttaaccgcaagaacaagttgctcttaataaagaaactctcggttc 1328  
 QY 609 aacgggttgcaaaagggtgtcaacttactatgaataatcgtccactagaattttcca 668  
 Db 1329 aacgggttgcaaaagggtgtcaacttactatgaataatcgtccactagaattttcca 1388  
 QY 669 cgttaagaatccaattatggaacaaccaagttccaccagcagcggtatttlaactgaat 728  
 Db 1389 cgttaagaatccaattatggaacaaccaagttccaccagcagcggtatttlaactgaat 1448  
 QY 729 accatccatcagtggtttgtgatagtttactacttaggtactactaactgtgtgttcg 788  
 Db 1449 accatccatcagtggtttgtgatagtttactacttaggtactactaactgtgtgttcg 1508  
 QY 789 tattgtcagtttaacgaattttgacgaagaagactttttaaaacacgtccaagattaca 848  
 Db 1509 tattgtcagtttaacgaattttgacgaagaagactttttaaaacacgtccaagattaca 1568  
 QY 849 atgttcaagcgttatctctgtacacgacttgtttgcaacttctaataagaagtgtaact 908  
 Db 1569 atgttcaagcgttatctctgtacacgacttgtttgcaacttctaataagaagtgtaact 1628  
 QY 909 cgaataaatgtatttcaaatattagttgaattgtgacatctgacgagacacttatactaa 968  
 Db 1629 cgaataaatgtatttcaaatattagttgaattgtgacatctgacgagacacttatactaa 1688  
 QY 969 agaaattgttgaagcgtgtgtcagaagctttaaataccgggtgtgtcgaagctatgtg 1028  
 Db 1689 agaaattgttgaagcgtgtgtcagaagctttaaataccgggtgtgtcgaagctatgtg 1748  
 QY 1029 ttttaacagaacaacactctgtcaattatccacacgggaaggagatgaataaccaggtgc 1088  
 Db 1749 ttttaacagaacaacactctgtcaattatccacacgggaaggagatgaataaccaggtgc 1808  
 QY 1089 ttctggcaaaagtgtgtccattatttaagaacaaagttalcgactctgtgatactaaaaaaac 1148  
 Db 1809 ttctggcaaaagtgtgtccattatttaagaacaaagttalcgactctgtgatactaaaaaaac 1868  
 QY 1149 ttgtggcccggaagaacggtgggaagttgtgttaagggtcctatgtctatgaagtgta 1208  
 Db 1869 ttgtggcccggaagaacggtgggaagttgtgttaagggtcctatgtctatgaagtgta 1928  
 QY 1209 tgttagtaaatccagaagcaacaagaataatcatagatgaagaaggtgtgtgtcacacag 1268  
 Db 1929 tgttagtaaatccagaagcaacaagaataatcatagatgaagaaggtgtgtgtcacacag 1988  
 QY 1269 agatattgggtattacgatgaagaataacattcttatacgttgcgttgaagtcctt 1328  
 Db 1989 agatattgggtattacgatgaagaataacattcttatacgttgcgttgaagtcctt 2048  
 QY 1329 aatcaaatataaagaatataagttaccacgtgtgaattagaatctgtcttttgaaca 1388  
 Db 2049 aatcaaatataaagaatataagttaccacgtgtgaattagaatctgtcttttgaaca 2108

QY 1389 tccaaatattttgtagtcggcggtgtgtgagttccagatccataagctgtgagcttc 1448  
 Db 2109 tccaaatattttgtagtcggcggtgtgtgagttccagatccataagctgtgagcttc 2168  
 QY 1449 gggagcgtgtgttacttaagaagaataatcatagcgtgaagaagaagtaagtgta 1508  
 Db 2169 gggagcgtgtgttacttaagaagaataatcatagcgtgaagaagaagtaagtgta 2228  
 QY 1509 cgttgcctgaagtttccaaatgcaaaacgtttgtcgtgtgtgtccgttttggagcga 1568  
 Db 2229 cgttgcctgaagtttccaaatgcaaaacgtttgtcgtgtgtgtccgttttggagcga 2288  
 QY 1569 agtacctaaaggtctcactgtgttaaatgtacgtgaagaacattagaagaataactgaagaa 1628  
 Db 2289 agtacctaaaggtctcactgtgttaaatgtacgtgaagaacattagaagaataactgaagaa 2348  
 QY 1629 accagttgctaagatg 1644  
 Db 2349 accagttgctaagatg 2364

## RESULT 13

AAK25717 standard; cDNA to mRNA; 1656 BP.

AAK25717;

21-MAY-1999 (first entry)

Firefly Luciferase gene #3.

Bioluminescent protein; catalytic efficiency; stability; firefly;

Luciferase; chimeric; Luciola cruciata; Luciola lateralis;

Photinus pyralis; primer; PCR; amplification; ss.

Chimeric - Luciola lateralis.

Chimeric - Photinus pyralis.

MO9902697-A1.

21-JAN-1999.

30-JUN-1998; 98WD-JP02936.

08-JUL-1997; 97US-0051917.

(KIKK ) KIKKOMAN CORP.

Hirokawa K, Kajiyama N, Murakami S;

WPI: 1999-120898/10.

P-PDB: AAW99366.

Example 3; Page 30-31; 53pp; Japanese.

The invention relates to the generation of bioluminescent proteins with improved catalytic efficiency and stability. The proteins are generated by addition, deletion or substitution of amino acids from a precursor protein e.g. firefly luciferases, or by constructing chimeric luciferase proteins from luciferase genes from e.g. Luciola cruciata, L. lateralis and Photinus pyralis. This sequence represents an example of a chimeric luciferase gene of the invention.

Sequence 1656 BP; 529 A; 283 C; 366 G; 478 T; 0 other;

Query Match 90.7%; Score 1490.4; DB 20; Length 1656;  
 Best Local Similarity 94.7%; Pred. No. 0;  
 Matches 1542; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 1 atggaaacatggaacgatgaaatatgtgatgttcctgaacacatttaccctatt 60  
1 atggaacacatggaacgatgaaatatgtgatgttcctgaacacatttaccctatt 60  
QY 61 gaagaaggatctgctgtgagcaacaattgcgaagtataatgatgatgataaacttga 120  
61 gaagaaggatctgctgtgagcaacaattgcgaagtataatgatgatgataaacttga 120  
QY 121 gcaattcctttacttaacgacctaccggtgttgatttaactgcgcgaactacttaaa 180  
121 gcaattcctttacttaacgacctaccggtgttgatttaactgcgcgaactacttaaa 180  
QY 181 aaatcatgctgtctagaggaaggctttaaagaatatgtgttgtgttgaaggaagt 240  
181 aaatcatgctgtctagaggaaggctttaaagaatatgtgttgtgttgaaggaagt 240  
QY 241 gcgtatgacgttgaagaactgtgaagaattcttattcctgttaataagccggttattta 300  
241 gcgtatgacgttgaagaactgtgaagaattcttattcctgttaataagccggttattta 300  
QY 301 ggtgtcggtgtggtcccaactgaagattacactctagctgaattgttccacagttta 360  
301 ggtgtcggtgtggtcccaactgaagattacactctagctgaattgttccacagttta 360  
QY 361 ggcactctaaagccaacaattgtatattagttctaaaaaaagatagataaagtataact 420  
361 ggcactctaaagccaacaattgtatattagttctaaaaaaagatagataaagtataact 420  
QY 421 gtacaaaaaaagcgaactgctcatataaacattgttatattgtgacagaagaagtgtattat 480  
421 gtacaaaaaaagcgaactgctcatataaacattgttatattgtgacagaagaagtgtattat 480  
QY 481 agaggttatcaatcgcacatgacacttataataaaaaaacacccaaggttccaagga 540  
481 agaggttatcaatcgcacatgacacttataataaaaaaacacccaaggttccaagga 540  
QY 541 tcaagttttaaaactgtagaagtttaaccgcaagaagaagttgctcttaataatgaactct 600  
541 tcaagttttaaaactgtagaagtttaaccgcaagaagaagttgctcttaataatgaactct 600  
QY 601 tcgggttcaaacgggtttggcaaaagggtgtgaacttctctgaataataatcgtcactaga 660  
601 tcgggttcaaacgggtttggcaaaagggtgtgaacttctctgaataataatcgtcactaga 660  
QY 661 tttctcaagctagaagatcccaattatgaaaccaagtttaccacagcgactatttta 720  
661 tttctcaagctagaagatcccaattatgaaaccaagtttaccacagcgactatttta 720  
QY 721 actgtatgacatcctcaatcgaattgtgtgtgtgtgttacttacttagctactacttgt 780  
721 actgtatgacatcctcaatcgaattgtgtgtgtgtgttacttacttagctactacttgt 780  
QY 781 gatttgcgtatgtcatgttgaagaatttgaagaagaagactttttaaaaaactgtcaa 840  
781 gatttgcgtatgtcatgttgaagaatttgaagaagaagactttttaaaaaactgtcaa 840  
QY 841 gattacaagtgttcaagcgttatctgttgaagcactgttgttgaatcttaataagaagt 900  
841 gattacaagtgttcaagcgttatctgttgaagcactgttgttgaatcttaataagaagt 900  
QY 901 gaattactcgataataatgatatcaaatattagttgaattgcatctgcgcgagcact 960  
901 gaattactcgataataatgatatcaaatattagttgaattgcatctgcgcgagcact 960  
QY 961 ttatctaaagaattgttgaagcgtgtgtgttagagttttaaattacggggtgtcgttaa 1020  
961 ttatctaaagaattgttgaagcgtgtgtgttagagttttaaattacggggtgtcgttaa 1020  
QY 1021 ggcctatggtttaacagaacaacctctgcaatttataccacccggaagcgatgataaa 1080  
1021 ggcctatggtttaacagaacaacctctgcaatttataccacccggaagcgatgataaa 1080

QY 1081 ccaagtgctctctgcaaaagttgtgccaatttattlaagcaaaagttatcgatcttgatact 1140  
1081 ccaagtgctctctgcaaaagttgtgccaatttattlaagcaaaagttatcgatcttgatact 1140  
QY 1141 aaaaaaactttggcccgcaagaacgtgtgagaagtttgtttaaagggtcctatgcttct 1200  
1141 aaaaaaactttggcccgcaagaacgtgtgagaagtttgtttaaagggtcctatgcttct 1200  
QY 1201 aaagtgtatgataatccgaagaacgaagaatacatagatgaagaagttgtgtg 1260  
1201 aaagtgtatgataatccgaagaacgaagaatacatagatgaagaagttgtgtg 1260  
QY 1261 cacaagaagatattggtlaltacgaatgaagaaaaacattcttaltatcgtgatcgtttg 1320  
1261 cacaagaagatattggtlaltacgaatgaagaaaaacattcttaltatcgtgatcgtttg 1320  
QY 1321 aagctttaatcaataaagaagatataaagttaccactctgttgatttgatcgttctt 1380  
1321 aagctttaatcaataaagaagatataaagttaccactctgttgatttgatcgttctt 1380  
QY 1381 ttgcaacatccaataatttttgatgcccgtgtgttcggttccagatccctatagctgt 1440  
1381 ttgcaacatccaataatttttgatgcccgtgtgttcggttccagatccctatagctgt 1440  
QY 1441 gagcttccggagagctgtgtgtacttaagaagaatactatgactgataaagaagta 1500  
1441 gagcttccggagagctgtgtgtacttaagaagaatactatgactgataaagaagta 1500  
QY 1501 atgattacgttgcgttagcgaagtttcaaatgcaaacgttgcgtgtgtgtgtcgtttt 1560  
1501 atgattacgttgcgttagcgaagtttcaaatgcaaacgttgcgtgtgtgtgtcgtttt 1560  
QY 1561 gtggaaggaagtaaccttaagcgtcactgttaaatltgacggtttaaagcaattagaagaata 1620  
1561 gtggaaggaagtaaccttaagcgtcactgttaaatltgacggtttaaagcaattagaagaata 1620  
QY 1621 ctgaagaa 1628  
1621 ctgaagaa 1628  
Db 1621 ctcaataa 1628

RESULT 14  
ID AAN91170 standard; DNA; 1644 BP.  
XX AAN91170;  
AC AAN91170;  
XX 14-JUN-1990 (first entry)  
DT 14-JUN-1990 (first entry)  
XX Recombinant luciferase gene.  
DE Recombinant luciferase gene.  
KW Luciferase; ATP assay; ss.  
XX Luciferase; ATP assay; ss.  
OS Luciola cruciata.  
XX Luciola cruciata.  
FN EP301541-A.  
XX EP301541-A.  
PD 01-FEB-1989.  
XX 01-FEB-1989.  
PE 28-JUL-1988; 88EP-0112233.  
XX 28-JUL-1988; 88EP-0112233.  
PR 29-JUL-1987; 87JP-0187724.  
XX 29-JUL-1987; 87JP-0187724.  
PR 29-JUL-1987; 87JP-0187725.  
XX 29-JUL-1987; 87JP-0187725.  
PR 20-AUG-1987; 87JP-0205194.  
XX 20-AUG-1987; 87JP-0205194.  
PA (KIKK ) KIKKOMAN CORP.  
XX (KIKK ) KIKKOMAN CORP.  
PI Masuda T, Tatsumi H, Nakano E;  
XX Masuda T, Tatsumi H, Nakano E;  
DR WPI: 1989-033443/05.  
XX WPI: 1989-033443/05.  
DR P-PSDB; AAP94367.  
XX P-PSDB; AAP94367.  
PT Recombinant luciferase gene - used for efficiently producing luciferase

PT In E. coli, obtaining a stable and highly active prod.  
 XX  
 PS Claim 2; fig 3; 35pp; English.

CC The sequence was obt'd. from cDNA prep'd. from mRNA isolated from  
 CC L. cruciata tails. The DNA can be incorporated into vectors for  
 CC transformation of E. coli JM 1010.  
 XX

SQ Sequence 1644 BP; 529 A; 276 C; 338 G; 501 T; 0 other;

Query Match 82.6%; Score 1357.6; DB 10; Length 1644;  
 Best Local Similarity 89.1%; Pred. No. 0;  
 Matches 1465; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

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QY 1 atggaacaatgagagcaatgaaatattgtgtatgtgtccctaaacatttcctatt 60
Db 1 atggaacaatgagagcaatgaaatattgtgtatgtgtccctaaacatttcctatt 60
QY 61 gaagaggatctgtgagagcaatgtgcgaagatatagtatgataatgaaattgga 120
Db 61 gaagaggatctgtgagagcaatgtgcgaagatatagtatgataatgaaattgga 120
QY 121 gcaattctttaaagcaactaccggtgctcgattatagcgcgcgaatactgaa 180
Db 121 gcaattctttaaagcaactaccggtgctcgattatagcgcgcgaatactgaa 180
QY 181 aaatcatgctctagagagagcttaagaatatagtgtgtgtgtatgagagaatt 240
Db 181 aaatcatgctctagagagagcttaagaatatagtgtgtgtgtatgagagaatt 240
QY 241 gcaatgagagagagagagagagagagagagagagagagagagagagagagag 300
Db 241 gcaatgagagagagagagagagagagagagagagagagagagagagagagag 300
QY 301 ggttcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 360
Db 301 ggttcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 360
QY 361 ggcattctaaagcaaatgttatgtcttaaaaaagagatagataaagtataact 420
Db 361 ggcattctaaagcaaatgttatgtcttaaaaaagagatagataaagtataact 420
QY 421 gtacaaaaacggttaactgtatataaaacattgttatgtgacacaaagtgtat 480
Db 421 gtacaaaaacggttaactgtatataaaacattgttatgtgacacaaagtgtat 480
QY 481 agaggtatcaatccatgagacaactttataaaaaaacacacacaaagtgttca 540
Db 481 agaggtatcaatccatgagacaactttataaaaaaacacacacaaagtgttca 540
QY 541 tcaagttttaaactgtagaagttaacgcgcaaaagaagaagtgtcttataatga 600
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QY 601 tcgggttcaaacggttggcaaaaggtgtgcaacttaactctgaataatcgtcactga 660
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Db 661 ttcttcacgctagagatccaattatagaaacaaagtttcaacgagcagcgtttta 720
QY 721 actgagagacattccatcagatgtttgtgtatgtttactaattagctactaactgt 780
Db 721 actgagagacattccatcagatgtttgtgtatgtttactaattagctactaactgt 780
QY 781 gatttcgattgtcatgttaacgaatattgaacgaagagactttttaaacaactgaa 840
Db 781 gatttcgattgtcatgttaacgaatattgaacgaagagactttttaaacaactgaa 840
QY 841 gattacaacgttcaacgcttattctgttacgagacttgtttgaattcttaataaga 900
Db 841 gattacaacgttcaacgcttattctgttacgagacttgtttgaattcttaataaga 900

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Db 841 gattataaagtcacaagtgattatctctgtaccgacttgtgtgcaattctcaacaaagt 900
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Db 901 gaattactcgataaataatgattatcaaaattgaattgaattgcattcgtgcgagacact 960
QY 961 ttatcaaaagaattgtgaaagctgtgtgtaagcgttttaattacccgggtgttcgtcaa 1020
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QY 1021 ggcattgtttaacagaacaacctctgcaattatatacaacgcggaagcgatataa 1080
Db 1021 ggcattgtttaacagaacaacctctgcaattatatacaacgcggaagcgatataa 1080
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Db 1081 ccagtgcttctggcaaatgtgtccattatataagcaaaagtgtatcgacttgatact 1140
QY 1141 aaaaaacttggccgcgacagacgtgagagaagttgtgtaaagggtctctatg 1200
Db 1141 aaaaaacttggccgcgacagacgtgagagaagttgtgtaaagggtctctatg 1200
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Db 1201 aaagttatgtatgaataccagaagcaacaagaataatcagatgaagaaggtgtgtg 1260
QY 1261 cacacggagatattggtatcagatgaagaagaacacattcttattcgtgagatcgttg 1320
Db 1261 cacacggagatattggtatcagatgaagaagaacacattcttattcgtgagatcgttg 1320
QY 1321 aagctttaaatacaatacaagaagataatcaagtaaccacgtcgtgaattagaatcgttct 1380
Db 1321 aagctttaaatacaatacaagaagataatcaagtaaccacgtcgtgaattagaatcgttct 1380
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QY 1621 ctgaagaacacagttgctaagatg 1644
Db 1621 ctgaagaacacagttgctaagatg 1644

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RESULT 15  
 AAQ03801  
 ID AAQ03801 standard; cDNA; 1644 BP.

XX AAQ03801;  
 AC 22-AUG-1990 (first entry)  
 DT 26-FEB-1993 (revised entry)  
 XX Recombinant luciferase gene.  
 DE  
 KW Luciferase; ATP; E. coli; photon; ds.  
 OS Synthetic.  
 XX JP02065780-A.  
 PN 06-MAR-1990.  
 PD

XX 01-SEP-1988; 88JP-0216229.  
 PF 01-SEP-1988; 88JP-0216229.  
 PR (KIKK ) KIKKOMAN CORP.  
 PA WPI: 1990-113360/15.  
 DR P-PSDB: AAR05788.  
 XX  
 PT Prepn. of luciferase -  
 using *Escherichia* sp. bacteria contg. recombinant DNA.  
 XX  
 PS Claim 2: Page 416 + Fig 3; 20pp; Japanese.  
 CC Prepn. of luciferase comprises culturing *Escherichia* sp. contg.  
 CC recombinant DNA, and harvesting luciferase from the culture medium.  
 CC The recombinant DNA is a vector DNA into which has been inserted the  
 CC luciferase gene which has the nucleotide sequence below. Luciferase  
 CC can be produced quickly and efficiently with an increased photon  
 CC output, useful in assaying ATP.  
 XX  
 SQ Sequence 1644 BP: 529 A; 276 C; 338 G; 501 T; 0 other;

Query Match 82.6%; Score 1357.6; DB 11; Length 1644;  
 Best Local Similarity 89.1%; Pred. No. 0;  
 Matches 1465; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 1 atggaacaatgagagaaacgaatgaaatattgtgtatgtcctgaaccattaccctatt 60  
 Db 1 atggaacaatgagagaaacgaatgaaatattgtgtatgtcctgaaccattaccctatt 60  
 QY 61 gaagggagatcgcgtgagacacattgcgcaagtatatgatgatcgatgacaaattgta 120  
 Db 61 gaagggagatcgcgtgagacacacacattgcgcaagtatatgatgatcgatgacaaattgta 120  
 QY 121 gcaattgctttactaacgacattacccgtgtcgattatlaagtaacgcaatactatgaa 180  
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 Db 361 ggcattcttaagcccaacattgtattgttcttaaaaaagagatagataaagttaact 420  
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 Db 421 gtacaaaaacgtaacgctatataaacattgttatattggaagaagaattgatatat 480  
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 Db 481 agagattatcaatcattggaacatttataaaaaaacattccacaaaggtttcaagaa 540  
 QY 541 tcaagtttaaaactgttgaagatttaacgcaagaagaagaagttgctcttataatgaactc 600  
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 QY 601 tcgagttcaaacggtttgcaaaaaaggtgtgcaacttactatgaaataatgtaactga 660  
 Db 601 tcgagttctaacggtttgcaaaaaaggtgtgcaacttactatgaaataatgtaactga 660

QY 661 tttctcacgctagagatccaaatttattggaaccagaatttcaccagcgatattta 720  
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 QY 1201 aaggttatgataatccagaagaacacagaagaataatgataagaaagttgtgtg 1260  
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Search completed: September 6, 2002, 19:39:15  
 Job time: 10803 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 19:29:53 ; Search time 113.65 Seconds  
(without alignments)  
3553.203 Million cell updates/sec

Title: US-09-581-241-5  
Perfect score: 1644  
Sequence: 1 atggaacaatgagagacga.....agaacacagttgtaagatg 1644

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/1na/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/1na/PCFUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/1na/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1636	99.5	1644	US-07-903-047-7	Sequence 7, Appli
2	1636	99.5	1644	US-09-111-752-13	Sequence 13, Appli
3	1636	99.5	1644	US-09-380-061B-15	Sequence 15, Appli
4	1628.2	99.0	1908	US-08-460-934-8	Sequence 8, Appli
5	1628.2	99.0	1908	US-08-782-118-8	Sequence 8, Appli
6	1619.6	98.5	1704	US-08-460-934-5	Sequence 5, Appli
7	1619.6	98.5	1704	US-08-782-118-5	Sequence 5, Appli
8	1357.6	82.6	1644	US-07-675-211-1	Sequence 1, Appli
9	1357.6	82.6	1644	US-07-903-047-1	Sequence 1, Appli
10	1357.6	82.6	1644	US-08-076-042-1	Sequence 1, Appli
11	1357.6	82.6	1644	US-08-757-046A-3	Sequence 3, Appli
12	1357.6	82.6	1644	US-09-447-208-3	Sequence 3, Appli
13	1357.6	82.6	1644	US-09-135-988-3	Sequence 3, Appli
14	1357.6	82.6	1644	US-09-277-716-3	Sequence 3, Appli
15	1357.6	82.6	1644	US-08-597-274A-3	Sequence 3, Appli
16	1357.6	82.6	1644	US-09-380-061B-13	Sequence 13, Appli
17	1264.8	76.9	1656	US-09-111-752-8	Sequence 8, Appli
18	1042.4	63.4	1656	US-09-111-752-6	Sequence 6, Appli
19	1042.4	63.4	1656	US-09-111-752-9	Sequence 9, Appli
20	1014.4	61.7	2009	US-09-380-061B-17	Sequence 17, Appli
21	817.2	49.7	1725	US-09-380-061B-19	Sequence 19, Appli
22	747.4	45.5	5427	US-09-282-996-2	Sequence 2, Appli
23	746.8	45.4	1811	US-08-867-352-22	Sequence 22, Appli
24	746.8	45.4	5789	US-08-862-431-32	Sequence 32, Appli
25	746.8	45.4	5791	US-08-862-431-31	Sequence 31, Appli
26	746.8	45.4	5793	US-08-862-431-29	Sequence 29, Appli
27	746.8	45.4	5793	US-08-862-431-30	Sequence 30, Appli

28	746.8	45.4	5818	US-08-536-559A-3	Sequence 3, Appli
29	746.8	45.4	5819	US-08-536-559A-2	Sequence 2, Appli
30	746.8	45.4	5819	US-08-862-431-27	Sequence 27, Appli
31	746.8	45.4	5819	US-08-862-431-28	Sequence 28, Appli
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34	746.8	45.4	6092	US-08-862-431-26	Sequence 26, Appli
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37	745.2	45.3	1650	US-08-354-240A-1	Sequence 1, Appli
38	745.2	45.3	2445	US-08-122-520C-8	Sequence 8, Appli
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45	745.2	45.3	6044	PCT-US95-12642-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1  
US-07-903-047-7  
; Sequence 7, Application US/07903047  
; Patent No. 5229285  
; GENERAL INFORMATION:  
; APPLICANT: Kajiyama, Naoki  
; APPLICANT: Nakano, Eiichi  
; TITLE OF INVENTION: Thermostable Luciferase of Firefly,  
; TITLE OF INVENTION: Thermostable Luciferase Gene of Firefly, No. 5229285el Reco  
; TITLE OF INVENTION: DNA And Process For The Preparation Of Thermostable  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/903,047  
; FILING DATE: 19920623  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7005-048  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1644 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: cDNA to mRNA  
; US-07-903-047-7

Query Match 99.5%; Score 1636; DB 1; Length 1644;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 atggaacaatgagaaacgataaataatgtatgtatgtcctgaaccatttaccctatt 60  
 Db 1 ATGGAACAATGAGAAACGATGAAATATGTGTATGTGTCCTGACCATTTTACCTATT 60  
 QY 61 gaagaggagatctgtcgtgagacaaatgtgcgaagtataatgatacgaatgaacttga 120  
 Db 61 GAAGAGGAGATCTGTCGTGAGACAAATGTGCCAAGTATATGATGATGCAAAACTTGA 120  
 QY 121 gaaattgtcttactaaagcacttcgggtgtcgtatgaatgaatgaatgaatgaatga 180  
 Db 121 GAAATTTGCTTTACTTACCCACTTACCGGTGTGATTAACGTACGCCAATATCTTAGA 180  
 QY 181 aataatgctgtctaggaagagccttaagaataatgattgtgtgtgtgtgtgtgtgtgt 240  
 Db 181 AATATGCTGTCTAGGAGAGGCTTTAAGAAATATGATGTTGTGTGTGTGTGTGTGTGT 240  
 QY 241 ggcgtatgcaatgaaactgtgaaagaatcttattctcgtatgaatgaatgaatgaatga 300  
 Db 241 GCGTATGCAATGAAACTGTGAAAGATCTTATTCCTGATTAAGCCGTTTATTTATA 300  
 QY 301 ggtgtcgt 360  
 Db 301 GGTGTGCGT 360  
 QY 361 ggcacatctaaagcaacaatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat 420  
 Db 361 GGCATCTCTAAAGCCAAATGTATTTAGTTTGTAAAAAGATTTAGATTAAGTTTAACT 420  
 QY 421 gtacaaaaaagtgtaactgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgt 480  
 Db 421 GTACAAAAAGCGTAACGTCTATTAACCATTTGTATTTGTGACGCAAGGTGATTTAT 480  
 QY 481 agagtttcaatcactgtgacaaacttataaataaacaacacacacacacacacacacacac 540  
 Db 481 AGAGTTTCAATCCTGATGACAACTTTATTAATAAAAAAACCTCCACAAAGTTTCAAGGA 540  
 QY 541 tcaagttttaaactgtgaagttaacccgaagaacaaagtgtgtgtgtgtgtgtgtgtgtgt 600  
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 QY 601 tcgggttcaacccgt 660  
 Db 601 TCGGTTCAACCCGTTTGTGCAAAAGGTGTGCAACTTACCAATGCAATGCACTCTAGA 660  
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 Db 661 TTTTCTCAAGGTGAGATGCAATTTATGAAACCAAGTTTACCAAGCAAGCGCTATTTTA 720  
 QY 721 actgtatgacatccatcactatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 780  
 Db 721 ACTGTATGACCATTCATCATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780  
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 Db 781 GTTTCTGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGT 840  
 QY 841 gattacaatgttcaagcgttattctgtacacgaatgtgtgtgtgtgtgtgtgtgtgtgtgt 900  
 Db 841 GATTACAATGTTCAGCGTTATCTTGTACCGACTTGTGTGCAATTTTATATGAAAT 900  
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 Db 961 TTATTTAAGAAATGTGTGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020  
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 Db 1021 GGCATTGTGTTAAGAAACAAACCTCTGCAATTTATTTATACACGCGAAGCATGATATAA 1080  
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Db 1081 CCAGTGCTCTTGCAAAAGTTGTGCATTTATTAAGCAAAATTTTCATCTGTGATCT 1140  
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 QY 1201 aaagttatgtatataatccagaagaagaagaatataatgaatgaatgaatgaatgaatga 1260  
 Db 1201 AAAGTTATGTAGATATATCCAGAAGCAACAGAAATCATATGATGATGAAGGTGTGTG 1260  
 QY 1261 cacacagagataatgtgtatcagaatgaagaacacatttcttactcgtgtatcgtgt 1320  
 Db 1261 CACACAGAGATATGTGTGATTAACATGAAGAAACATTTCTTTATCTGTGATCTGTG 1320  
 QY 1321 aagtttatacaatacaagaagataatcaatgaacacgtgtgtgtatgaatgtatgt 1380  
 Db 1321 AAGTCTTATATCAAAATCAAGAGATATCAAGTACCACTGTGTAATTAAGATCTGTCTT 1380  
 QY 1381 ttgcaacatccaaataatgtgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440  
 Db 1381 TTGCAACATCCAAATATTTTGTGATGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
 QY 1441 gagcttccggagcgt 1500  
 Db 1441 GAGCTTCCGGAGCGT 1500  
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 Db 1501 ATGATTTAGTTGT 1560  
 QY 1561 gtggacgaagtaacciaaagctcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1620  
 Db 1561 GTGGACGAAGTACTTAAGCTCTCACTGTAAATTTGACGTTAAAGCAATTTAGAGAAATA 1620  
 QY 1621 ctgaagaaacccagttgtcgaagt 1644  
 Db 1621 CTGAAGAAACCAAGTTGTCTAAGATG 1644

RESULT 2  
 US-09-111-752-13  
 ; Sequence 13, Application US/09111752  
 ; Patent No. 6074859  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HITOKAWA, KOZO  
 ; APPLICANT: KAJIYAMA, NOKI  
 ; TITLE OF INVENTION: MUTANT-TYPE BIOLUMINESCENT PROTEIN, AND  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSER: OBLON, SPIVAK, MCLELLAND, MATER & NEUBAUER,  
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
 ; CITY: ARLINGTON  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/111,752  
 ; FILING DATE: 08-JUL-1998  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: OBLON, NORMAN F.  
 ; REGISTRATION NUMBER: 24,618  
 ; REFERENCE/DOCKET NUMBER: 7126-0009-0  
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ. ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1644 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 ORIGINAL SOURCE:  
 ORGANISM: *Luciola lateralis*  
 US-09-111-752-13

Query Match 99.5%; Score 1636; DB 3; Length 1644;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 atggaacacatggaacacatggaacatggtatggtcctgaaccattaccatt 60  
 DB 1 ATGGAACACATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 60  
 QY 61 gaagaggatctgctggaacacatggaacatggtatggtcctgaaccattaccatt 120  
 DB 61 GAAGAGGATCTGCTGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 120  
 QY 121 gcaatgcttctgaacacatggaacacatggtatggtcctgaaccattaccatt 180  
 DB 121 GCAATGCTTCTGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 180  
 QY 181 aaatcagctgctggaacacatggaacacatggtatggtcctgaaccattaccatt 240  
 DB 181 AAATCAGCTGCTGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 240  
 QY 241 gcatgctgctggaacacatggaacacatggtatggtcctgaaccattaccatt 300  
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 DB 421 GTACAAAACATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 480  
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 DB 481 AGAGGTATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 540  
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 DB 541 TCAAGTTTGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 600  
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 DB 781 GGTTCCTGAGTGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 840

QY 841 gattacaacatggaacacatggaacacatggtatggtcctgaaccattaccatt 900  
 DB 841 GATTACAACATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 900  
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 DB 901 GAATTCTGAACATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 960  
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 DB 961 TTATCTGAACATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 1020  
 QY 1021 ggcattcctggaacacatggaacacatggtatggtcctgaaccattaccatt 1080  
 DB 1021 GGCATTCTGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 1080  
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 DB 1081 CCAAGGTCCTGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 1140  
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 DB 1141 AAAAAACATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 1200  
 QY 1201 aaaggtatggaacacatggaacacatggtatggtcctgaaccattaccatt 1260  
 DB 1201 AAAGGTATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 1260  
 QY 1261 cccacaggaacatggaacacatggaacacatggtatggtcctgaaccattaccatt 1320  
 DB 1261 CCCACAGGAACATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 1320  
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 DB 1321 AAGTTCCTGAACACATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 1380  
 QY 1381 ttgcaacatggaacacatggaacacatggtatggtcctgaaccattaccatt 1440  
 DB 1381 TTGCAACATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 1440  
 QY 1441 gagctcctggaacacatggaacacatggtatggtcctgaaccattaccatt 1500  
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 DB 1501 ATGGTATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 1560  
 QY 1561 gtgacgaacatggaacacatggaacacatggtatggtcctgaaccattaccatt 1620  
 DB 1561 GTGACGAACATGGAACACATGGAACATATGTGTATGTCCTGACCATTTACCTATT 1620  
 QY 1621 ctgaagaacacatggaacacatggtatggtcctgaaccattaccatt 1644  
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RESULT 3  
 US-09-380-061B-15  
 Sequence 15, Application US/09380061B  
 Patent No. 6265177  
 GENERAL INFORMATION:  
 APPLICANT: SOUIRELL, DAVID JAMES  
 WHITE, PETER JOHN  
 LOWE, CHRISTOPHER ROBIN  
 MURRAY, JAMES AUGUSTUS HENRY  
 TITLE OF INVENTION: ENZYME ASSAY FOR MUTANT FIREFLY LUCIFERASE  
 NUMBER OF SEQUENCES: 21  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHYE P. C.  
 STREET: 1100 NORTH GLEBE ROAD  
 CITY: ARLINGTON

```

STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/380,061B
  FILING DATE: 25-Aug-1999
  CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCY/GB98/01026
  FILING DATE: 7-APR-1998
  APPLICATION NUMBER: GB 9707468.8
  FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
  NAME: SADOFF, B. J.
  REGISTRATION NUMBER: 36,663
  REFERENCE/DOCKET NUMBER: 124-725
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (703)816-4100
  TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 15:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1644 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: both
    TOPOLOGY: both
  MOLECULE TYPE: CDNA
  FEATURE:
    NAME/KEY: CDS
    LOCATION: 1..1644
    SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-380-061B-15

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Query Match 99.5%; Score 1636; DB 4; Length 1644;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1639; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 361 GGCATCTCTTAAGCCAAACATGTATTTAGTTCTTAATAAAAGATAGATTAAGTTATAACT 420
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Db 1321 AAGCTTTTATTAATTAACAAAGATATCAAGTACCACTGCTGAATTTAGAACTGTGTTCT 1380
QY 1381 ttgcaacatccaaatatttttgaatgcggcggttgcgttccagatccctataactgt 1440
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Db 1381 TTGCAACATCCAAATATTTTATGATCCGGCGTTGTGGGGTTCCAGATCCCTATACCTG 1440
QY 1441 gagcttccggagagcgtgtgtgttacttaagaagaanaactctatgactgaagaagta 1500
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Db 1441 GAGCTTCCGGGAGCGTGTGTTGTTACTTGAAGAAAGAAATCTATGACGAAAAAAGTA 1500
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QY	1081	ccaagtgtctcttgccaagtltgtccattatattaagcnaaaagttatcgatctgtact	1140
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QY	1141	aaaaaaacttgggccccgaacagaacgttggagaagtttgttaaaaggttcctagtctatg	1200
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QY	1201	aaagtatattgataataccagaagcaacaaagagaatcatagatgtaagaagttgtgttg	1260
Db	1201	aaagtattattgatatattccagaagcaacaaagagaatcatatgattgaacagaagttgttg	1260
QY	1261	cacacaggaagatatctgggtattacagatgaagaanaacattcttctatcgttgatcgttgg	1320
Db	1261	caacacaggaagatttttgggtattacagatgaamaaaaaacatttcttattcgttgatcgttgg	1320
QY	1321	aagttctttaaacaatacaagaagatcaagttacacacctgtgaatttgaatctgttctt	1380
Db	1321	aagttctttaaacaatacaagaagatcaacgatatccacacctgtgaatttgaatctgttctt	1380
QY	1381	ttgcaaatccaaatatcttttgaatgcggcgttgtgtgctgtccagatccctaagtctgt	1440
Db	1381	ttgcaaatccaaatatatttttttgatgcggcgcttgcgtgcgattccagatcccttattagctggt	1440
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QY	1621	ctgagaagaacccagtgtctaag	1641
Db	1621	ctgagaagaacccagtgtctaag	1641

RESULT 5  
US-08-782-118-8  
; Sequence 8, Application US/08782118  
; Patent No. 5843746  
; GENERAL INFORMATION:  
; APPLICANT: TATSUMI, HIROKI  
; APPLICANT: FUKUDA, SATOSHI  
; APPLICANT: KIKUCHI, MAMORU  
; APPLICANT: KOYAMA, YASUJI  
; TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE  
; TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A  
; TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT  
; TITLE OF INVENTION: ANALYSIS METHOD  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
; ADDRESS: P.C.  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/782,118
3 FILING DATE: 13-JAN-1997
4 CLASSIFICATION: 435
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: US 08/460,934
7 FILING DATE: 05-JUN-1995
8 APPLICATION NUMBER: JP 193798/1994
9 FILING DATE: 27-JUL-1994
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: JP 54625/1995
12 FILING DATE: 14-MAR-1995
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: JP 98857/1995
15 FILING DATE: 24-APR-1995
16 ATTORNEY/AGENT INFORMATION:
17 NAME: OBLON, NORMAN F.
18 REGISTRATION NUMBER: 24,618
19 REFERENCE/DOCKET NUMBER: 7126-001-0
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: 703-413-3000
22 TELEFAX: 703-413-2220
23 INFORMATION FOR SEQ ID NO: 8:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 1908 base pairs
26 TYPE: nucleic acid
27 STRANDEDNESS: double
28 TOPOLOGY: unknown
29 MOLECULE TYPE: DNA (genomic)
30 FEATURE:
31 NAME/KEY: misc feature
32 LOCATION: 1..1908
33 OTHER INFORMATION: /note="The nucleotide sequence of
34 OTHER INFORMATION: the biotinylated firefly luciferase gene contained in
35 OTHER INFORMATION: recombinant plasmid pRLf248 DNA"
36 FEATURE:
37 NAME/KEY: CDS
38 LOCATION: 1..1908
39 US-08-782-118-8

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RESULT 6  
 US-08-460-934-5  
 ; Sequence 5, Application US/08460934  
 ; Patent No. 5814465  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TATSUMI, HIROKI  
 ; APPLICANT: FUKUDA, SATOSHI  
 ; APPLICANT: KIKUCHI, MAMORU  
 ; APPLICANT: KOYAMA, YASUJI  
 ; TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE  
 ; TITLE OF INVENTION: FOR BIOTINYLATED FIREFLY LUCIFERASE, A RECOMBINANT DNA, A  
 ; TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESSEE: P.C.  
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
 ; CITY: ARLINGTON  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/460, 934  
 ; FILING DATE: 05-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 193798/1994  
 ; FILING DATE: 27-JUL-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 54625/1995  
 ; FILING DATE: 14-MAR-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 98857/1995  
 ; FILING DATE: 24-APR-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: OBLON, NORMAN F.  
 ; REGISTRATION NUMBER: 24,618  
 ; REFERENCE/DOCKET NUMBER: 7126-001-0  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 703-413-3000  
 ; TELEFAX: 703-413-2220  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1704 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: DNA (genomic)  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 1..1704  
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 ; OTHER INFORMATION: /note= "Nucleotide sequence of the

OTHER INFORMATION: biotinylated firefly luciferase gene contained in recombinant  
OTHER INFORMATION: plasmid pHL203 DNA\*  
US-08-460-934-5

Query Match 98.5%; Score 1619.6; DB 1; Length 1704;  
Best Local Similarity 99.4%; Pred. No. 0;  
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RESULT 7  
US-08-782-118-5  
Sequence 5, Application US/08782118  
Patent No. 5843746  
GENERAL INFORMATION:  
APPLICANT: TATSUHI, HIROKI  
APPLICANT: FUKUDA, SATOSHI  
APPLICANT: KIKUCHI, MAMORU  
APPLICANT: KOYAMA, YASUJI  
TITLE OF INVENTION: BIOTINYLATED FIREFLY LUCIFERASE, A GENE  
TITLE OF INVENTION: PROCESS FOR PRODUCING BIOTINYLATED AND A BIOLUMINESCENT  
TITLE OF INVENTION: ANALYSIS METHOD  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P. C. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk



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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/782,118
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/460,934
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: JP 193798/1994
FILING DATE: 27-JUL-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 54625/1995
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 98857/1995
FILING DATE: 24-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 7126-001-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
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NAME/KEY: misc.feature
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OTHER INFORMATION: /note= "Nucleotide sequence of the
OTHER INFORMATION: biotinylated firefly luciferase gene contained in recombinant
OTHER INFORMATION: plasmid pHLf203 DNA"
US-08-782-118-5

Query Match 98.5% Score 1619.6 DB 2: Length 1704;
Best Local Similarity 99.4% Pred. No. 0;
Matches 1625; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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## RESULT 8

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US-07-675-211-1
: Sequence 1, Application US/07675211
: Patent No. 5219737
:
: GENERAL INFORMATION:
:   APPLICANT: KAJIYAMA, NAOKI
:   APPLICANT: NAKANO, EIICHI
:   TITLE OF INVENTION: MUTANT LUCIFERASE OF A FIREFLY, MUTANT
:   TITLE OF INVENTION: LUCIFERASE GENES, NOVEL RECOMBINANT DNAs CONTAINING THE
:   TITLE OF INVENTION: GENES AND A METHOD OF PRODUCING MUTANT LUCIFERASE
:   NUMBER OF SEQUENCES: 4
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: PENNIE & EDMONDS
:   STREET: 1155 AVENUE OF THE AMERICAS
:   CITY: NEW YORK
:   STATE: N.Y.
:   COUNTRY: U.S.A
:   ZIP: 10036
:
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.25
:   CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/07/675,211
:   FILING DATE: 19910326
:
: CLASSIFICATION: 435
:
: ATTORNEY/AGENT INFORMATION:
:   NAME: MISROCK, S. LESLIE
:   REGISTRATION NUMBER: 18,872
:   REFERENCE/DOCKET NUMBER: 7005-026-999
:   TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 212-790-9090
:   TELEFAX: 212-869-9741
:   TELEX: 66141 PENNIE
:
: INFORMATION FOR SEQ ID NO: 1:
:   SEQUENCE CHARACTERISTICS:
:   LENGTH: 1644 base pairs
:   TYPE: NUCLEIC ACID
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:   MOLECULE TYPE: cDNA
:   ORIGINAL SOURCE:
:   ORGANISM: Luciola cruciata
:   FEATURE:
:   NAME/KEY: CDS
:   LOCATION: 1...1644
:
: US-07-675-211-1

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Query Match	82.68;	Score 1357.6;	DB 1;	Length 1644;
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Best Local Similarity 89.1%; Pred. No. 0;  
Matches 1465; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

**D**

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Db	1141	aaaaaatcttttagtccctaacacgacgtggagaaattgtttaaagctcctatgctatg	1201
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1 RESULT 10
2 US-08-076-042-1
3 ; Sequence 1, Application US/08076042
4 ; Patent No. 5330906
5 ; GENERAL INFORMATION:
6 ;
7 APPLICANT: KAJIYAMA, NAOKI
8
9 APPLICANT: NAKANO, EIICHI
10
11 TITLE OF INVENTION: MUTANT LUCIFERASE OF A FIREFLY, MUTANT
12
13 TITLE OF INVENTION: LUCIFERASE GENES, NOVEL, RECOMBINANT DNAS CONTAINING THEM
14
15 TITLE OF INVENTION: GENES AND A METHOD OF PRODUCING MUTANT LUCIFERASE
16
17 NUMBER OF SEQUENCES: 4
18
19 CORRESPONDENCE ADDRESS:
20
21 ADDRESSEE: PENNIE & EDMONDS
22
23 STREET: 1155 AVENUE OF THE AMERICAS
24
25 CITY: NEW YORK
26
27 STATE: N.Y.
28
29 COUNTRY: U.S.A
30
31 ZIP: 10036
32
33 COMPUTER READABLE FORM:
34
35 MEDIUM TYPE: Floppy disk
36

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1  COMPUTER: IBM PC compatible
2  OPERATING SYSTEM: PC-DOS/MS-DOS
3  SOFTWARE: Patentin Release #1.0, Version #1.25
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/08/076,042
6  FILING DATE: 15-JUN-1993
7  CLASSIFICATION: 435
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: US 07/675,211
10 FILING DATE: 26-MAR-1991
11
12 NAME: 435
13
14 ATTORNEY/AGENT INFORMATION:
15 NAME: MISROCK, S. LESLIE
16 REGISTRATION NUMBER: 18,872
17 REFERENCE/DOCKET NUMBER: 7005-026-999
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: 212-790-9090
20 TELEFAX: 212-869-9741
21
22 TELEX: 66141 PENNIE
23
24 INFORMATION FOR SEQ ID NO. 1:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 1644 base pairs
27 TYPE: nucleic acid
28 STRANDEDNESS: single
29 TOPOLOGY: linear
30 MOLECULE TYPE: CDNA
31 ORIGINAL SOURCE:
32 ORGANISM: Luciola cruciata
33
34 FEATURE:
35 NAME/KEY: CDS
36 LOCATION: 1..1644
37
38 US-08-076-042-1

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Query Match	82.6%	Score 1357.6	DB 1	Length 1644
Best Local Similarity	89.1%	Pred. No. 0		
Matches 1465	Conservative	0	Mismatches 179	Indels 0
				Gaps 0
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Oy	61 gaagsgagatcgtcgtgagcaacattgcgcgaagatatagagtcgatgatgcaaaactgga	120		
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Oy	121 gcaattgcttttactcaagcaactaccggtgtgcgattatacgtacgcgaacttagaa	180		
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Oy	181 aatcatcgtcgtcgtgagagagcctttaaagaattatggttggttgcgtgatggaagt	240		
Db	181 AATCATGTGTGCTTAGGAAAAAGCTTTGCAAAATTATGTGTTGGTTGTTGATGCGCAAA	240		
Oy	241 gcatatgcaatgaaaacctgtgaaqaattcttattccgtatagaccggttattata	300		
Db	241 GCGTATGACAGTGAAGAACTGTGAAGAATTTTATTTCGTAAATGACCGGACTGTTTATA	300		
Oy	301 ggtgtcgtgtgtgcgtccaactaaatgagattacactcaactcaagtgaattggttcaagttta	360		
Db	301 GGTGTGCTGTGTGCCACCACTAATGAGATTTAACCTTTACGTAACGTGTTCCACAGTTTA	360		
Oy	361 ggcattcttaagccaacaaattgtaattgcttctaataaagaattagataaagttataact	420		
Db	361 GGTATCTCTTAACCAACAACTGTATTATTAGTCTTAAAAAGGCTTAAAGATTATTAACA	420		
Oy	421 gtacaaaaaagtgtaacgtcatataaaacaattgtlatatggaacaagaatgagattat	480		
Db	421 GTACGAAAAACGTAACACTATTTAACCAACTGTATTACTAGATGAGGAAGTTCATTAT	480		
Oy	481 agaggtatcaatccatbgaacaacttataaaaaaaacactccaagaattccaaga	540		
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TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...1644  
OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)  
PUBLICATION INFORMATION:  
US-09-447-208-3

Query Match 82.6%; Score 1357.6; DB 3; Length 1644;  
Best Local Similarity 89.1%; Pred. No. 0;  
Matches 1465; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

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Db 181 AAATCATGCTGCTGAGCAAAAGCTTTGCAAAATATGCTGCTGCTGCTGCTGCTGCTG 240  
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RESULT 13  
US-09-135-988-3  
Sequence 3, Application US/09135988  
Patent No. 6152358  
GENERAL INFORMATION:  
APPLICANT: Bryan, Bruce  
TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe  
STREET: 4250 Executive Square, 7th Floor  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette





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RESULT 14  
 US-09-277-716-3

; Sequence 3, Application US/09277716A  
 ; Patent No. 6232107  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bryan, Bruce  
 ; APPLICANT: Szent-Gyorgyi, Christopher  
 ; APPLICANT: PROLUME, LTD.  
 ; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE  
 ; CURRENT FILING DATE: 1999-03-26  
 ; EARLIER FILING DATE: 1998-10-01  
 ; EARLIER FILING DATE: 1998-06-15  
 ; EARLIER FILING DATE: 1998-03-27  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1644  
 ; TYPE: DNA  
 ; ORGANISM: Luciola cruciata  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1644)  
 ; OTHER INFORMATION: Luciola cruciata (firefly) Luciferase  
 ; PUBLICATION INFORMATION:  
 ; PATENT DOCUMENT NUMBER: 4,968,613  
 ; PATENT FILING DATE: 1988-07-26  
 ; PUBLICATION DATE: 1990-11-06  
 ; US-09-277-716-3

Query Match 82.6%; Score 1357.6; DB 4; Length 1644;  
 Best Local Similarity 89.1%; Pred. No. 0;  
 Matches 1465; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

Qy 1 atggaacacatgaggaacgatgaataatattgtgtatgtgtcctgaaccatttaccctatt 60  
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Db 1261 CACACCGAGATTTGGATATTATGATGAAAGAAACATTTCTTATTTGATCGATTG 1320
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Db 1321 AAGCTTTAATCAAAATACAAAGGATACCAAGTACCACCTGCCGATTTAGAATCGTCTT 1380
QY 1381 ttgcaacatccaataattttgatgcccgcgttgctggtccagatccctatacgtgt 1440
Db 1381 TTGCAACATCCATCTTATCTTTGATGTGTGCGCGCTTCTCTGATCCTGTAGCTGGC 1440
QY 1441 gagcttcgagagctgtgtgtgtacttaagaagaagaatctatgactgaagaagaagta 1500
Db 1441 GAGCTTCCAGAGCGCGTTGTGTGTTACTGGAAGCGGAAAAATATGACCGAAAAAGAACTA 1500
QY 1501 atggaattacgttgctagtaagttcaaatgcaaaacgtttgcgtggtgtgtgtgt 1560
Db 1501 ATGGAATTATGTTGCAAGTCAAGTTTCAATGCAAAACGTTTACGTGTGTGTGTGTGT 1560
QY 1561 gtgagcgaagtaacctaaagtcctactggttaaaattgacggtlaaagcaattagagaata 1620
Db 1561 GTGATGTAAGTACCTTAAGGCTTACTGGAATAAATGACGCGACAGCAATTAGAGAAATC 1620
QY 1621 ctgaagaanaaccagttgctaaagtg 1644
Db 1621 CTTAAGAAACCACTTGTCTAAGATG 1644
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Search completed: September 6, 2002, 19:30:28  
Job time: 15191 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: September 6, 2002, 17:47:30 ; Search time 3537.97 Seconds  
(Without alignments)  
6271.674 Million cell updates/sec

Title: US-09-581-241-5  
Perfect score: 1644  
Sequence: 1 atggaacacatgagacga.....agaacacagctgctaagatg 1644

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

## Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	208.6	12.7	664	10 C83857	C83857 C83857 Dict
2	199.4	12.1	768	10 BM412281	BM412281 EST586608
3	198.2	12.1	667	9 A1486799	A1486799 EST245121
4	190.4	11.6	651	10 C90519	C90519 C90519 Dict
5	189.8	11.5	582	9 AW621420	AW621420 EST312218
6	185.8	11.3	625	9 A1485586	A1485586 EST243907
7	183.2	11.1	569	9 AW218471	AW218471 EST303654
8	181.6	11.0	522	9 A1488821	A1488821 EST247160
9	173.8	10.6	543	10 BE555239	BE555239 SP87A10.Y
10	173.6	10.6	612	10 BG130282	BG130282 EST475938
11	171.8	10.5	606	10 BI923203	BI923203 EST543107
12	165.6	10.1	741	9 AU214129	AU214129 AU214129
13	162.4	9.9	535	9 AL389862	AL389862 MCB57H09
14	162.2	9.9	498	10 B1425803	B1425803 sah72f03.
15	162.2	9.9	570	10 BG791252	BG791252 ESTFN115
16	161.4	9.8	548	10 BM188336	BM188336 saj39f03.
17	159.4	9.7	604	9 AU219684	AU219684 AU219684

18	159.4	9.7	604	9 AV558307	AV558307 AV558307
19	158.8	9.7	520	10 B1269977	B1269977 NF003D02F
20	158.8	9.7	638	9 AU214473	AU214473 AU214473
21	158.2	9.6	712	9 AW349844	AW349844 GM210006A
22	158	9.6	611	10 B1129072	B1129072 B1129072
23	157.8	9.6	644	10 B1309413	B1309413 EST530823
24	157.8	9.6	722	10 B139943	B139943 B139943
25	157.6	9.6	590	9 AW329421	AW329421 N200656
26	157.4	9.6	558	9 AV680327	AV680327 AV680327
27	157.4	9.6	567	10 BG580544	BG580544 EST4832271
28	157.4	9.6	656	9 AW691106	AW691106 NF041C085
29	154.8	9.4	410	10 BM109695	BM109695 EST557231
30	154.8	9.4	977	12 CNS01MDU	AL150803 Anopheles
31	152.2	9.3	808	9 AW348381	AW348381 GM210002A
32	150.2	9.1	540	9 A1771202	A1771202 EST52398
33	149.6	9.1	506	9 AW132800	AW132800 se10d11.Y
34	149.2	9.1	529	10 BM143081	BM143081 saj39c03.
35	148.8	9.1	377	9 A1938631	A1938631 sb56d11.Y
36	148.8	9.1	655	9 AW560940	AW560940 EST315988
37	148.6	9.0	453	10 BF005122	BF005122 EST433620
38	148.6	9.0	495	9 AJ284477	AJ284477 4A3B-AAx-
39	147	8.9	683	10 BF492687	BF492687 AT01136.3
40	146.2	8.9	565	10 BR330067	BR330067 s073a05.Y
41	145.8	8.9	665	10 BF200141	BF200141 WHE2232_E
42	145.8	8.9	665	10 BF200141	BF200141 WHE2232_E
43	145	8.8	595	9 AW329094	AW329094 N200300e
44	144.6	8.8	623	10 BF634495	BF634495 NF062B09D
45	144.4	8.8	501	10 BG882703	BG882703 sae51e04.

## ALIGNMENTS

RESULT 1  
LOCUS C83857 664 bp mRNA linear EST 28-APR-1999  
DEFINITION C83857 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium  
DISCOIDEUM cDNA clone SSA391, mRNA sequence.  
ACCESSION C83857  
VERSION C83857.1 GI:2706789  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum.  
ORGANISM Dictyostelium discoideum  
REFERENCE  
AUTHORS Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mitra,B.N., Pl.M., Saito,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,T., Ochiai,H. and Tanaka,Y.  
The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of development  
JOURNAL DNA Res. 5 (6), 335-340 (1998)  
MEDLINE 99156227

TITLE  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan  
Email: d402nuesakura.cc.tsukuba.ac.jp  
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'  
POLYA-No. Location/Qualifiers

FEATURES  
source  
1..664  
/organism="Dictyostelium discoideum"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="SSA391"  
/clone\_lib="Dictyostelium discoideum SS (H.Urushihara)"  
/dev\_stage="slug"  
BASE COUNT 234 a 105 c 124 g 201 t  
ORIGIN

Query Match 12.7%; Score 208.6; DB 10; Length 664;



Db	752	GAAGTGAGGATTCAT	768
RESULT	3		
LOCUS	A1486799	667 bp	mRNA linear
DEFINITION	EST245121 tomato ovary, TMU Lycopersicon esculentum cDNA clone		
ACCESSION	A1486799		
VERSION	A148679.1	GI:4382170	
KEYWORDS	EST.		
ORGANISM	Lycopersicon esculentum		
REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliopsida: eudicotyledons: core eudicots: Asteridae: euasterids I; Solanales; Solanaceae; Solanum;		
AUTHORS	Lycopersicon. 1 (bases 1 to 667) Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Romling,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nieman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J.		
TITLE	Generation of ESTs from tomato carpel tissue		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a> .		
FEATURES	Location/Qualifiers		
SOURCE	1..667 /organism="Lycopersicon esculentum" /cultivar="TA496" /db_xref="taxon:4081" /clone="cLED1D3" /clone_lib="tomato ovary, TAMU" /tissue_type="carpel" /dev_stage="5 days pre-anthesis to 5 days post-anthesis" /lab_host="X14-Blue MR" /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; cLED - Tomato Carpel EST Library. Oligo(dT)-primed and directionally cloned cDNA in vector lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."		
BASE COUNT	201 a	120 c	155 g
ORIGIN			191 t

Query Match	12.1%	Score 198.2	DB 9	Length 667
Best Local Similarity	57.6%	Pred. No. 3.2e-35		
Matches 384	Conservative 0	Mismatches 266	Indels 15	Gaps 1
QY	838	caagatlaacaaatgltcaagcgatattcctgtgaccgaattglttgcaattcctaataga	897	
DB	1	CAAAATTTACAAAGTACCACTAAGGGCCATTGTGGCCACCATTGTTTGGCATATTTCTAAG	60	
QY	898	agtgaattactcgataatataatcattacaattagttgaaattgcatctgcgcgagca	957	
DB	61	ACTCCATGCGTTGATTAATATTATTTATCATGTGGTAAGAACCCTATGTGCGGCTGCA	120	
QY	958	ccttattctaaagaattggtgaagctgtgtctagaagtttaatttaccggtgttcgt	1017	
DB	121	CCATTATGGAAGAACTTGTAAGACACTGTTCCAGGCCAAATTTCTTAATCTTAACTTGCT	180	
QY	1018	caagcgatcgtgttcaacaganaaacaccttcgaattatattacacacgcgaaagcgatga	1076	
DB	181	CAAGGTTACGGAATGCACAGACCAGCAAGTGTGGCTATGTGCTATGGCATTTGCTANA	240	
QY	1077	-----taaccagtgcttccttgccaagtgtgcctattttaaagcaaaa	1122	
DB	241	GAAACCTTGGAATTTAAATCTTGAGCATGTGGACACTGTTGTAAGAAATCTGATGATGA	300	

Oy	1123	gttaccggtctctgtatacctcaaaaacctcttggcccgaaagaagctgggaagtttgtta	1182
Db	301	ATTGTGGATCTCTGATACACTGGCAATCTCTCCCTAGAGAACCAATCTGGAGAGATTTGTATA	360
Oy	1183	aagggtccctatgtctatgaagaagtlatgtatagataaatccagaagcaacaagaagaaatcata	1242
Db	361	AGAGGCGATCAAAATTATGAAGTGTACTTAATATGATCCAGAGGCCACTACG6GGAACATA	420
Oy	1243	gattgaagaagaatttggtctgcacacaggaatatgtgtatcttaacgatgaagaaaaacatttc	1302
Db	421	GACCAAGAAAGGTGGTTTCATACGGGCGCATATGTGTTTATTGAAATCGATGATGAGCTT	480
Oy	1303	tttatctggaatcgcgtttgaagtcctttaatcaataacaagaatatcaaatccacactgct	1362
Db	481	TTTCATTGTGGATCGTTTAAAGSAAATTGATAAATATCAAAAGSATTTCAGTG6GCTCTGCT	540
Oy	1363	gaattagaatctgtctctcttgcacaatccaaatatctttgatctgcgcygctgttggcgtt	1422
Db	541	GAACTTTGAAGCCCTCTCTCCTCATCATCCCAATATTTCAGATGCTGCTGTGTTTCATAG	600
Oy	1423	ccagatccctatagctgtgttgagctctcccggaagctgtgtttgttaacttaagaagaagaaatct	1482
Db	601	AAAGGCGAGCAAGCGAGGAAGTCTCTGTCGTGTTTGTTCAGATCAAAAGGCTCCACA	660
Oy	1483	atgactgt 1489	
Db	661	ATTACTG 667	

	RESULT	4	
	LOCUS	C90519	
	DEFINITION	C90519 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium	EST 20-APR-1998
	ACCESSION	C90519	
	VERSION	C90519.1	GI:3060139
	KEYWORDS	EST.	
	SOURCE	Dictyostelium discoideum.	
	ORGANISM	Dictyostelium discoideum	
	REFERENCE	Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.	
	AUTHORS	1 (bases 1 to 651)	
	TITLE	Morito,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshino,R., Mita,B.N., Pl.M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.	
	JOURNAL	Developmental cDNA in Dictyostelium discoideum	
	COMMENT	Unpublished (1998)	
	FEATURES	Contact: Hideto Urushihara Institute of Biological Sciences University of Tsukuba 3-3-10 Ten-noda, Tsukuba, Ibaraki 305, Japan Email: d402hu@sakura.cc.tsukuba.ac.jp. Location/Qualifiers 1..651 /organism="Dictyostelium discoideum" /strain="AX4" /db_xref="taxon:44689" /cclone="SS1661" /clone_lib="Dictyostelium discoideum SS (H.Urushihara)" /dev_stage="slug"	
	BASE COUNT	251 a                 83 c                 110 g                 207 t	
	ORIGIN		
QY	Query Match	11.6%;	Score 190.4; DB 10; Length 651;
	Best Local Similarity	62.6%;	Pred. No. 2e-33;
	Matches 313; Conservative	0; Mismatches 186; Indels 1; Gaps 11;	
QY	1117	gcacaaagtatcgaattatactaacaaacttggcccgcaagacggtgagaagtc	1176
Db	1	GCCTAAATCATCTCTTCACAGACTGGTGGAATTGCGTAAGGCGAANAAGGTGAATC	60
QY	1177	tgttgtaaggctctatgcttatgaaaggtatgatgatacatcgaagaacaagaaga	1236

FEATURES	SOURCE
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/organism="Lycopersicon esculentum"	
/cultivar="TA496"	
/db_xref="taxon:4081"	
/clone="cLEX11N8"	
/clone_lib="tomato root during/after fruit set, Cornell University"	
/tissue_type="root"	
/dev_stage="plants during and after fruit-set"	
/note="Vector: pBluescript SK(-): Site 1: EcoRI, Site 2: XhoI; supplier: Tankley; tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."	
181 a	99 c 146 g 156 t

Query Match	Similarity	11.5%	Score	No. 8:	DB 9:	Length	582:		
Best Local	Similarity	60.6%	Pred	No. 2:	6e-33:				
Matches	330:	Conservative	0:	Mismatches	212:	Indels	3:	Gaps	1
OY	1079	aaccagatgcttcctggcaaaagtgtgcacattttaagaacaagaatcatcgaatcttgata	1138						
Db	2	AATCGAGGGGCATGTGGTACCTGTTGAGAACGACAGATGAATAATTGGATCCCGATA	61						
OY	1139	cfaaaaaactttggcccccgaacgaagcgagggaagtgttgtlaaaggcttctatgcta	1198						
Db	62	CGGGTTGCTCTCTGCCCTTAACAACCACCGGTGAATTTTGCAATTGAGGTGATCAAAATGA	121						
OY	1199	tgaaggttatcttagataaatccaagaacaagaagaatactagatgaagaagtttgt	1258						
Db	122	TGAAGAGTTACTTGAATGATGCCCTGAAGCTACAGCTAGAACAMTAGAAAAAAGAAGATGCT	181						
OY	1259	tgcacacagagatatattggtgtatctacgatggaagaaaacattcttarcgttgtatcgt	1318						
Db	182	TACACACTGGCAGATTGGATATTGACAGATGATGATGAGCTTTTCATCGTGAGATCGAT	241						
OY	1319	tgaagctcttaataataacaagaagatcatcaagtcaccctgtgaatagatcgttc	1378						
Db	242	TGAAGGAATTGATCAATATCAAAGATTTCAAGTGGCGCTGCTGATACCTGGAACCTTC	301						
OY	1379	tttgcacatccaaataattttgatlbcocgcgttgtcgtlccagatccatagctg	1438						
Db	302	TGTCAACACACCCCTTAACATTTTCGATGTCGTGCTGTGTCCTCATGAAGAATGAACACGG	361						
OY	1439	gtgagctctccggagactgtgtgttgcacttaagaagaagaacctatgctgtaaaagaag	1498						
Db	362	GGAAGTTCATGCTGCTTTGTTGTTAGATCAAAATGATCTCACATTCATTCGATGAGATGAAG	421						
OY	1499	taatgattacgttgctagtcagtttcaatgcaaacgaacgcttgctggtgtgtgccgt	1558						
Db	422	TGAAGATTTCATCTCCCAAGCAGCGATATTCCTATAAGAAAT----AAGCGTATATTTT	478						
OY	1539	ttgtgacgaagtacctaagaagctctcaactggttaaattgaagcataagcaattagagaa	1618						
Db	479	TGCTGGAGACGGTACCGAAATCTCCATCAGAAAAATTCGTGAGAAAAGACTTAAGAGCTA	538						
OY	1619	tactg 1623							
Db	539	GACTG 543							
RESULT	6								
LOCUS	A1485586	625 bp	mRNA linear EST 18-MAY-2001						
DEFINITION	EST243907 tomato ovary, TMU Lycopersicon esculentum cDNA clone								
ACCESSION	A1485586								
VERSION	A1485586.1	GI:4380957							
KEYWORDS	EST.								
SOURCE	Lycopersicon esculentum								
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;								
REFERENCE	1 (bases 1 to 625)								
AUTHORS	Alcala,J., Vrebalov,J., White,R., Matero,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Romling,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nieman,W., Fraser,C.M., Ventier,J.C., Martin,G.B., Tanksley,S.D., and Giovannoni,J.								
TITLE	Generation of ESTs from tomato carpel tissue								
JOURNAL	Unpublished (1999)								
COMMENT	Contact: CUGI Clemson University Genomics Institute 100 Jordan Hall, Clemson, SC 29634, USA Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a> .								





LOCUS	A1488821	522 bp	mRNA	linear	EST-18-MAY-2001
DEFINITION	EST2742760 tomato ovary, TAMU Lycopersicon esculentum cDNA clone				
VERSION	CLED18L20	mRNA sequence.			
ACCESSION	A1488821				
KEYWORDS	A1488821.1	GI:4384192			
SOURCE	EST.				
ORGANISM	tomato.				
	Lycopersicon esculentum				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	Asteridae; euasterids I; Solanales; Solanaceae; Solanum;				
	Lycopersicon.				
REFERENCE	1 (bases 1 to 522)				
AUTHORS	Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Konning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J.				
TITLE	Generation of ESTs from tomato carpel tissue				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: CUGI				
	Clemson University Genomics Institute				
	Clemson University				
	100 Jordan Hall, Clemson, SC 29634, USA				
	Email: <a href="http://www.genome.clemson.edu/orders/index.html">http://www.genome.clemson.edu/orders/index.html</a> .				
FEATURES	Location/Qualifiers				
SOURCE	1..522				
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	/tissue_type="carpel"				
	/dev_stage="5 days pre-anthesis to 5 days post-anthesis"				
	/lab_host="XL1-Blue MR"				
	/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:				
	XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and				
	directionally cloned cDNA in vector Lambda ZAP II with 5'				
	and 3' ends located at the EcoRI and XhoI sites,				
	respectively."				
BASE COUNT	156 a	89 c	133 g	144 t	
ORIGIN					

Query Match	11.0%;	Pred. 181.6;	DB 9;	Length 522;
Best Local Similarity	62.6%;	Freq. No. 2e-31;		
Matches 283;	Conservative 0;	Mismatches 169;	Indels 0;	Gaps 0;
QY 1072	gataataaacacagcgcctctcgcaaaqcttgccattatcttaaagcaaaagtatcgat	1131		
Db 43	GATATTAAATCATCAGGGGCATGTGTACCGTTTGGAGGAACGCAGAGATCAAAATTGTGAT	102		
QY 1132	cttgactataaaaaaacttggcccgacagacagcttgagaagcttgctgtaaaagctct	1191		
Db 103	CCGGATACGGGGTGTCTCTCGCCCGTAACCAACCCGGTGAAATTTGGATTAGAGGTGAT	162		
QY 1192	atgcctatgaagaagcttatgctatgataatccacagaagcaacaagagaaatcatatgataagaa	1251		
Db 163	CAAAATCATGAAGGTGTACTTGTGATATACCCCTGAAGCTGACGTAGAACATATGAATAAAAGAA	222		
QY 1252	gcttgctgtgcacacagcagatatactgctatcagcttgagaagaaaacattcttatacgt	1311		
Db 223	GGATGGTTACACACTGGCGATTGTGGATATTTTGCGATGATGATGAGACCTTTTCATTCGCG	282		
QY 1312	gacgctttgaagctcttatacaaatcaacaagaagataatcaagtaacacccctgcgaattagaa	1371		
Db 283	GATCGATTGAAGGAATTGATCAATATACAAAGATTTCAAGTGGCCCTGCTGTAATCTGCA	342		
QY 1372	tctgctcttttgcaacatcacaataatttttgatgcgcgacgttgcctgctgctccagatcct	1431		
Db 343	GCACCTTCTGTCAACCAACCCCTAACCTTTCATGCTGCTGCTGTGTCACATGAAAGATGAA	402		
QY 1432	atagctgtgtgccttccgcgagcctgcttgcttacttaagaagaataatcatatgactgaa	1491		

D<sub>b</sub>    403 CAAGGGGAGAAGTCCAGTGCGCTTTTGTTGTAGATCAATGATCATACCAATTACTAG 462  
Q<sub>y</sub>    1492 aaagaagtaatgattacgttgcctagtcaagt 1523  
       | ||||| | ||||| |                  | || ||  
D<sub>b</sub>    463 GATGAAGTGAAGATTTCATCTTCAACAAGST 494

RESULT	9
BEE55239	
LOCUS	BEE55239
DEFINITION	spr7a10.y1 Gm-cl045 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl045-1995 5' similar to TR.O4868 O4868 4-COUARATE:COA LIGASE
ACCESSION	BEE55239
VERSION	2
KEYWORDS	mRNA sequence.
SOURCE	BEE55239.1 GI:3619726
ORGANISM	soybean. Glycine max

REFERENCE	AUTHORS
1 (bases 1 to 543)	Shoemaker, R., Kaim, P., Vockin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Riltter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterson, R. and Wilson, R.
TITLE	Public soybean EST Project
JOURNAL	Unpublished (1999)
COMMENT	Contact: Shoemaker R/Public Soybean EST Project

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
This clone is available through: ResGen, Thyltrogen Corp, 2130  
South Memorial Parkway Huntsville, AL 35801 For further information  
call: (800)-533-4363 or contact via email: [cu@resgen.com](mailto:cu@resgen.com)  
High quality sequence stop: 416.

FEATURES	SOURCE
Location/Qualifiers	1. .543
/organism="Glycine max"	
/db_xref="taxon:3847"	
/clone="GENOME SYSTEMS CLONE ID: Gm-c1045-595"	
/clone_id="Gm-c1045"	
/tissue_type="Hypocotyl, 9-10 day old etiolated seedlings"	
/lab_host="DH10B"	
/note="Vector: plusscriptII SK; Site.1: EcoRI; Site.2: XhoI; This cDNA library was constructed from mRNA isolated from etiolated hypocotyl tissue of 9-10 day old seedlings of the cultivar Williams 82. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) primer with a XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the plusscript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."	
BASE COUNT	184 a 92 c 130 g 137 t
ORIGIN	

Query Match	10.6%	Score 173.8	DB 10	Length 543
Best Local Similarity	59.0%	Pred. No. 1.3e-29		
Matches 317	Conservative	0	Mismatches 217	Indels 3
				Gaps 1
OY 1093	ggcgaagttg	gccatattta	aaagcaaa	gtatcgatccttgatacttaaaaaacttg 1152

Db 7 GGAACCGTTGTGAGAAACCGTGAAGATGAATCGTGATACAGAAACGGGTGATTCCTT 66  
 QY 1153 gcccgaacagacgctggagaagcttgtaagaaggtctcctatgataagagttatgta 1212  
 Db 67 CCAAGAAACAAATCCGAGAAATTTGATTAAGAGGGGCAAGGTCATGAAGAGATATCTA 126  
 QY 1213 gataatccagaagaacagagagaaatcatagatgaagaaggttggttgacacagagagt 1272  
 Db 127 AATGACCCAGAGGCTACAGAGACACTATTAAGACAGAGAGATGTTTACACACAGAGAT 186  
 QY 1273 attgggtatgaagtaagaacaaatcttctatcgttgatcgtttgaagctttaa 1332  
 Db 187 ATTGGTTTCATTGATGATGATATTAAGACTCTTCTGATGTCGTTAAAGGATGATC 246  
 QY 1333 aaatacaaaagatalcaagtlacacactctgtaagaatgcttcttcttgcaacatca 1392  
 Db 247 AATATCAAAAGGATTCAGAGAGCTCTGAGCTCGAAGCTTTGTTGATGCTACCCA 306  
 QY 1393 aatattttgatccgagctgtgctgctgctcagatccatagcttgtagcttcgcgga 1452  
 Db 307 AACATTTCTGATCTCGCTGTGATGATGAAGATGAAGCTGACAGAGAAATTCACATT 366  
 QY 1453 gctgttgcttactaagaagaagaatactatgactgaagaagaagtaatgatacgtt 1512  
 Db 367 GCATTTTGTGTAAGGTCAATGTTCTGAGATTACGAGAGATGAATTAAGACATACATT 426  
 QY 1513 gctagtcagttcacaatgcaaaacgttgcgtggtggtgctgcttcttgagcgaagta 1572  
 Db 427 TCACACACAGCTGCTATTTTCAAGAGAGATGATGAGATTTTC--TTACAGGACTCTATT 483  
 QY 1573 cctaaagctcactgctgtaaatgtaagcgtgaagaatgagaagaatgagaaga 1629  
 Db 484 CTTAAACGACCTTCGCGCAAAATTTCTCGAAGGATTAATCTGACACACTTAACGAA 540

RESULT 10  
 BG130292 612 bp mRNA linear EST 31-JAN-2001  
 LOCUS BG130292 tomato shoot/meristem Lycopersicon esculentum cDNA clone  
 DEFINITION EST475938 5' sequence, mRNA sequence.

ACCESSION BG130292  
 VERSION BG130292.1 GI:12630480  
 KEYWORDS EST.  
 SOURCE tomato.  
 ORGANISM Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.

REFERENCE 1 (bases 1 to 612)  
 AUTHORS van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T.,  
 Hansen, C., Roming, C. and Tanksley, S.  
 TITLE Generation of ESTs from tomato shoot/meristem tissue  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 Location/Qualifiers  
 1..612  
 location="Lycopersicon esculentum"  
 /organism="TA496"  
 /db\_xref="taxon:4081"  
 /clone="cTOF29J22"  
 /clone\_1id="tomato shoot/meristem"  
 /tissue\_type="shoot/meristem"  
 /dev\_stage="developing shoots from 4-6wks old plants"  
 /lab\_host="SOLR"  
 /note="Vector: pluscript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; Small expanding leaves from the growing tip were  
 taken from greenhouse plants (4-6wks old TA496). Tissue  
 was immediately frozen in liquid nitrogen."

FEATURES  
 source

1..612  
 location="Lycopersicon esculentum"  
 /organism="TA496"  
 /db\_xref="taxon:4081"  
 /clone="cTOF29J22"  
 /clone\_1id="tomato shoot/meristem"  
 /tissue\_type="shoot/meristem"  
 /dev\_stage="developing shoots from 4-6wks old plants"  
 /lab\_host="SOLR"  
 /note="Vector: pluscript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; Small expanding leaves from the growing tip were  
 taken from greenhouse plants (4-6wks old TA496). Tissue  
 was immediately frozen in liquid nitrogen."

BASE COUNT 189 a 104 c 137 g 182 t  
 ORIGIN

Query Match 10.6%; Score 173.6; DB 10; Length 612;  
 Best Local Similarity 61.8%; Pred. No. 1,4e-29;  
 Matches 294; Conservative 0; Mismatches 179; Indels 3; Gaps 1;

QY 1148 ctttgcccgagacagacgctggagaagcttgtaagaaggtcctatgataaggt 1207  
 Db 9 CTCTCCCGCTAACACCCGGTGAATTTGATGATGAGTGATCAATCAATGAAGGTT 68  
 QY 1208 atgtgataatccagaagaacaaagaagaatcatagatgaagaaggttggtgcacag 1267  
 Db 69 ACTTGAATGACCTTCAAGCTACAGCTACAGATGAAGAAAGAGATGTTACACCTG 128  
 QY 1268 gagatattgggtatcagatgaagaacaaatcttctatcgttgatcgtttgaagctt 1327  
 Db 129 GCGATATTGATATATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 188  
 QY 1328 taataaatacaagaatatacaagtlacacactctgtaagaatgatacgttcttgcaac 1387  
 Db 189 TCAATCAATTAACAAAGATTTCAAGTGGCGCTGCTGAAGCTGAGACTTCTTGCAAC 248  
 QY 1388 atccaataatttgatgctgagcgttgctgctgctcagatccatagcgttgagcttc 1447  
 Db 249 ACCCTAACATTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 308  
 QY 1448 cggagagctgttctgacttaagaagaagaatactatgactgaagaagaagtaagtt 1507  
 Db 309 CAGTGCTTTTGTGTTAGATCAAAATGATTCATCACTTCAAGATGATGAAGAGATT 368  
 QY 1508 acgttgctagtaagttcacaatgcaaaacgttgcgtggtggtgctgcttgtagacg 1567  
 Db 369 TCATCTCCAAGAGGTGATTTCTATAGACAAT--AAAGCTGTATTTTTCGTGAGA 425  
 QY 1568 aagtaacctaaagctcactgtaaatgtaagcgtgaagaagaatgagaatcgt 1623  
 Db 426 CGGTACCGAAATCTCATCAGCAAAATTTCTGAAAGACTTAAGAGCTAGACTG 481

RESULT 11  
 B1923203 606 bp mRNA linear EST 18-OCT-2001  
 LOCUS B1923203 tomato callus Lycopersicon esculentum cDNA clone  
 DEFINITION EST543107 5' end, mRNA sequence.

ACCESSION B1923203  
 VERSION B1923203.1 GI:16221846  
 KEYWORDS EST.  
 SOURCE tomato.  
 ORGANISM Lycopersicon esculentum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;  
 Lycopersicon.

REFERENCE 1 (bases 1 to 606)  
 AUTHORS Alcala, J., Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai,  
 J., Utterback, T., Van Aken, S., Roming, C.M., Fraser, C.M., Martin,  
 G.B., Tanksley, S.D. and Giovannoni, J.  
 TITLE Generation of ESTs from tomato callus tissue (2001)  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 This clone is available through the Clemson University Genomics  
 Institute  
 Seq primer: T3.  
 Location/Qualifiers  
 1..606  
 /organism="Lycopersicon esculentum"  
 /cultivar="TA496"

FEATURES  
 source

```

/db_xref="taxon:4081"
/clone="clec79H20"
/tissue_type="tomato callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRF"
/notes="Vector: Bluescript SK(-); Site:1: EcoRI; Site:2:
XhoI; Supplier: Boyce Thompson Institute; sequencing: The
Institute for Genomic Research; clec - Cotyledons of
seedlings 7-10 days post-germination were excised, cut at
both ends and placed at 25 and 40 days and included
callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST library"

BASE COUNT      207 a      84 c      138 g      177 t
ORIGIN

Query Match      10.5%; Score 171.8; DB 10; Length 606;
Best Local Similarity 57.1%; Pred. No. 3.7e-29;
Matches 342; Conservative 0; Mismatches 242; Indels 15; Gaps 1;

QY 790 atgtcatgttaacgaattgacgaagacattttaaaacacgcgaagtataca 849
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 6 ATCTTGGTTATGAGAATTTGATGTTGATGATGTTGATGTTGATGTTGATG 65

QY 850 tgtcaagcgtatctctgtacgcgaattgtgtcaattcttaataagaatla 909
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 GTCAAAATTTGACCTTTTGTACACCTATTAATTTTGGCTATTCCTAAAGTCA 125

QY 910 gataaataatattatcaaatatagtgaaatgcatcgtgaggaacattataa 969
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 126 GATATATTATGACTTTTATGATGATGATGATGATGATGATGATGATGATG 185

QY 970 gaattgtgaagcgtgtgtacgaatttcaattaccgggtgtgtgtcaagctat 1029
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 186 AAGCTTGAGAGGATGTTGAATTAATTTCTTAATGCTTAATGCTGATGCTGAT 245

QY 1030 ttaacaga-----aacacactcgcgaattatcatcacaccggaagcgat 1074
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 246 ATGACGAGGCGCGGTGACCTATTAACATGCTTGTAGCATTTGCCAAAAGAAC 305

QY 1075 gataaacaggtgtcttcgcgaagtggtcattatlttaagcaaaagtatcgat 1134
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 306 ATAAATCAGAGGCGATGTGACAGTATTAAGAAATGCTGAGTGAATTTGGAT 365

QY 1135 gatactaaaaaacttggccgaacagacgtgtgaagttgtgttaaaggtctat 1194
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 366 GATACCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 425

QY 1195 cttaataaagttatgtatgtaatacgaagcaacaaagaataatcatagatga 1254
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 426 ATTATGAAAGGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 485

QY 1255 tggctgcacacaggaatattgttattacgaatgaagaacatttcttcatcgt 1314
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 486 TGGTTACATAGTGGTATTAAGGCTATTAATTAAGATGATGATGATGATGAT 545

QY 1315 cgttgaagcttataatcaatacaagatatacgaatccacgtgtgaatgaatc 1373
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 546 CGATTAAAGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 604

RESULT 12
AUI14129/c 741 bp mRNA linear EST 17-JUL-2001
DEFINITION AUI14129 unpublished oligo-capped cDNA library, stage 12
Caenorhabditis elegans cDNA clone yk809105 3', mRNA sequence.
ACCESSION AUI14129
VERSION AUI14129.1 GI:14852286
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea

```

```

REFERENCE 1 : Rhabditidae; Peloderinae; Caenorhabditis.
AUTHORS Kohara,Y., Shin-I,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
TITLE A complementary view of the C.elegans genome
JOURNAL Unpublished (2001)
COMMENT Contact: Yoji Kohara
Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.

FEATURES
source
1..741
location/Qualifiers
/organism="Caenorhabditis elegans"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk809f05"
/clone_lib="unpublished oligo-capped cDNA library, stage
12"
/sex="Hermaphrodite"
/tissue_type="whole animal"
/dev_stage="L2"

BASE COUNT      216 a      158 c      125 g      241 t      1 others
ORIGIN

Query Match      10.1%; Score 165.6; DB 9; Length 741;
Best Local Similarity 57.6%; Pred. No. 1e-27;
Matches 357; Conservative 0; Mismatches 254; Indels 9; Gaps 3;

QY 1000 aattaccgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1059
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 694 AATTGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 635

QY 1060 acaccggaagcgtatgataaaccaggtgtc---tgcaaaagtgtgtccattt 1116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 634 CCTGATTTAAGAAATGATCAATGATGATGATGATGATGATGATGATGATG 575

QY 1117 gcaaaagtatcgtatcgtatcgtatcgtatcgtatcgtatcgtatcgtat 1176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 574 ATGAAGATTGTGGAAACGAGAACCGACAGAGAACCGGTTAACCAACGAGGA 515

QY 1177 tgttaaaaggtccctatgtaaaaggttatgtatgataatcgaagaagcaaga 1236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 514 TGTGTTGCGTCCACAAATTAATGCTTGTGATCTCGAAGACCAAGAACAC--AGCC 458

QY 1237 atcatagatgaagaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 457 AGCACTGTCATCGATGATGATGATGATGATGATGATGATGATGATGATG 398

QY 1297 catctcttatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1356
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 397 AATTGTTTATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 338

QY 1357 cctgtgaatgaagaatcgtgtcttcttgcacatccaaatatttgtgtccggtgt 1416
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 337 CCAGCTGAACCTTGAAAGATCTTCTCTATCTCATCTCAACAAAGATTAAGAT 278

QY 1417 ggcgttccagatccctatagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1476
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 277 GGAATCCAGATGCTTAAGCTGAGAAATTAACCTTAACCAATTTGTTGTA--AGAGCTGAT 221

QY 1477 aaatctatgactgaagaagaagaatgattgattgattgattgattgattgatt 1536
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 220 AACACTCTCACTGACAGAGAGATTAAGGACTTTGTTAAACCAAAAGTCTCTTACAAA 161

QY 1537 cgttgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1596
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 160 CAACTCGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 101

QY 1597 gacgttaagaacatgaaga 1616

```

Db 100 TTGAGACGATTCTTGAGAGA 81

RESULT 13  
AL389862

TGAGACGATCTTGAGACA 81

DEFINITION	MtBC57H09f1 MtBC Medicago truncatula cDNA clone MtBC57H09 T3, mRNA sequence.
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```

VERSION AL389862.1  GI:9689615
KEYWORDS EST.
SOURCE

```

ORGANISM      Medicago truncatula  
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

**AUTHORS**  
Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jallion, O.,  
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson,  
V. and Carreau, D.

TITLE	Medicago truncatula ESTs from endomycorrhizal roots
JOURNAL	Unpublished (2000)
COMMENT	Contact: Corcoran

genoscope - Centre National de séquençage  
BP 191 91006 EVRY cedex - France  
E-mail: [secret@genoscope.cns.fr](mailto:secret@genoscope.cns.fr) Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

CNRS-INDA BP 37 31326 Casparyat-Tollosan Cedex Franco (E-mail : [contact@pascal.garnas-et-ellenne-pascal.journet.laboiraire.de](mailto:contact@pascal.garnas-et-ellenne-pascal.journet.laboiraire.de))

```

/clone_lib="Gm-cl049"
/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="3 week old"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+. Site_1: EcoRI; Site_2:
XhoI; The Clark NTL was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Specht, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 3 week old greenhouse
grown plants. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site and a 3' anchor. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). The library was constructed
in cooperation with Dr. Paul Keim's laboratory at Northern
Arizona University."

```

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BASE COUNT      165 a      86 c      119 g      128 t
ORIGIN

```

```

Query Match      9.9%; Score 162.2; DB 10; Length 498;
Best Local Similarity 60.5%; Pred. No. 5.8e-27;
Matches 285; Conservative 0; Mismatches 183; Indels 3; Gaps 1;

QY 1159 aacagacgtgagaagttgtgtaagaagtcctatgataaagttatagataat 1218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 28 AACAAACACGGTGAATTTGCTATAGAGGCACAAAGCTCATATGATATTAATGAC 87

QY 1219 ccaagaagaacaagaatacatagataagaagttgtgtgacacagaagataattg 1278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 88 CCAGAGCTACAGAGACAGACTGACACAAAGAGATGCTTACACAGAGATTTGTT 147

QY 1279 tattaagtgagaagaacattcttattcgtgagtcgtttgaagtccttaacaat 1338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 148 TTCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 207

QY 1339 aagaatcatcaatgacacacgtcgtatgataatcgttcttgaacatcaatatt 1398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 208 AAAGATATTCCAAGTGGCTCCCTGCTAGCTGAGCATTTGTTATTTGCCACCCCAACATTT 267

QY 1399 ttgagtcgcgcgttgcgtgcgtccagatccatagctgtagctccgcgcgcgtt 1458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 268 TCTGATGCTGCGCTGTGTAGCATGAAGATGAAGCTGAGGGAATTCAGTTCATTT 327

QY 1459 gttgacttaagaagaataatctatgactgataaagaagtaattgattagttc 1518
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 328 GTTGTAAAGTCAAAATGTTCTGAGATCCCGAGATGAATCAAGAAATACATTTCACAA 387

QY 1519 caagttcaaatgcaaacglttgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1578
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 388 CAGGGGTTTTTTTACACAGAGATAGTAGAGTTTCTTTCACGGAGCTCTATTCCTTAA 444

QY 1579 ggtctactgttaaatgacgttaagaacaattagagaataactgaaga 1629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 445 GCACCCCTGAGGAAAATTTCTGGGAAAGTATTAACTGCAGACCTTAAGGAA 495

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RESULT 15
LOCUS      BG791252      570 bp      mRNA      linear      EST 16-MAY-2001
DEFINITION ESTFN115 Tomato Root Subtraction cDNA Library Lycopersicon
            esculentum cDNA clone 10D1 5' similar to 4-coumarate--CoA ligase 2a
            , mRNA sequence.
ACCESSION  BG791252
VERSION    BG791252
KEYWORDS   EST.
SOURCE     tomato.
ORGANISM   Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

```

```

REFERENCE
1 (bases 1 to 570)
AUTHORS   Wang, Y.-H., Garvin, D.F. and Kochian, L.V.
TITLE     Nitrate-Induced genes in tomato roots: array analysis reveals novel
          genes that may play a role in nitrogen nutrition
JOURNAL   Plant Physiol. 127 (1), 345-359 (2001)
MEDLINE   21437959
COMMENT   Contact: Kochian LV
          US Plant Soil & Nutrition Lab
          Cornell University
          Tower Rd, Ithaca, NY 14853, USA
          Tel: (607) 255-5445
          Fax: (607) 255-1132
          Email: lvk@cornell.edu
          Seq primer: 73

```

```

FEATURES
    source
        1..570
            Location/Qualifiers
                /organism="Lycopersicon esculentum"
                /cultivar="TA496"
                /db_xref="taxon:4081"
                /clone="10D1"
                /clone_lib="Tomato Root Subtraction cDNA Library"
                /tissue_type="Roots"
                /dev_stage="5 weeks"
                /note="Organ: Roots; Vector: pBluescript KS; Directional"

```

```

BASE COUNT      172 a      103 c      136 g      159 t
ORIGIN

```

```

Query Match      9.9%; Score 162.2; DB 10; Length 570;
Best Local Similarity 62.2%; Pred. No. 6e-27;
Matches 273; Conservative 0; Mismatches 163; Indels 3; Gaps 1;

QY 1185 ggtcctatgcttatagaaggtatgtagataatccagaagaacaagaatacataga 1244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 33 GGGTATCAAAATGATGAAGGTACTTGAACGACCCCTGAAGCTACAGTAACATAGA 92

QY 1245 tgaagaagttgtgtgacacagagagatatgtgtattacgataagaagaacattctt 1304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 93 AAAGAGAGATGTTTACACACCTGCGGATTTGGATATATTGACGATGATGAGACTTTT 152

QY 1305 tatcgtgacgttltgaagtccttaacaatacaagaagataatcaatgacacgtgtga 1364
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 153 CATCGTGAATGATGAAGGAATGATCAAAATGAAGATTTCAAGTGGCGCTGTGTA 212

QY 1365 attgaatcgttcttlttgcaacatccaaatatlttgatgcgcgcgttgcgcgttcc 1424
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DB 213 ACTCGAAGCACTTCTTGTCAACACCCCTTAACATTTCTGATGCTGTGTTGCCAATGAA 272

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DB 273 AGATGAACAAGGGGAGAGATTCCAGTGCTTTTGTGTATGATCAAAATGATGATCCACT 332

QY 1485 gactgaaaaagaagaatgattgactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 333 TACTGAGATGAAGTGAAGGATTTTCATCCCAAGCAGGATATTTCTAATAGAGAT--- 389

QY 1545 tgggtgtgcgttlttgtagcgaaggtacctaagaagtcactgttaaatgacgtgtaa 1604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 390 AAAGCGTGTATTTTCGTGGAGACGCTACCGAAATCTCATCAGGAAAAATTTCTGAGAA 449

QY 1605 agcaattagagaatactg 1623
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 450 AGACTTAAGAGCTAGACTG 468

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Search completed: September 6, 2002, 17:47:36  
 Job time: 9589 sec



